

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run On: May 16, 2001, 09:00:12 ; Search time 1134.01 Seconds
(without alignments)
10651.138 Million cell updates/sec

Title: US-09-402-488A-3
Perfect score: 819
Sequence: 1 ATCCGGGTCTCATCATCA.....ATTCCAACTGCACCCCTGTAG 819

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
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2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
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7: gb_om.*
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9: gb_pat1.*
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11: gb_ph.*
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86: gb_pr2.*
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88: gb_pr4.*
89: gb_pr5.*
90: gb_pr6.*
91: gb_pr7.*
92: gb_pr8.*
93: gb_pr9.*
94: gb_rol.*
95: gb_rol2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|---------------|-------|----------------|--------|----|---------------------------|
| 1 | 567 | 69.2 | 1164 | 8 | CYIGH M27000 Cyprinus ca |
| 2 | 528.6 | 64.5 | 1117 | 8 | AF069398 Carassius |
| 3 | 527 | 64.3 | 1158 | 8 | CCGH X13670 Cyprinus c |
| 4 | 509.4 | 62.2 | 1179 | 8 | AF069399 Carassius |
| 5 | 504 | 61.5 | 1158 | 8 | HNPGH X60473 H.nobilis (|
| 6 | 502.4 | 61.3 | 1170 | 8 | HMEGH X60475 H.multitrix |
| 7 | 501.4 | 61.2 | 567 | 8 | CAU28388 Carassius a |
| 8 | 500.8 | 61.1 | 1171 | 8 | CIPGH X60474 C.idellus (|
| 9 | 496 | 60.6 | 1171 | 8 | CTEGRH M27094 Ctenopharyn |
| 10 | 460.6 | 56.2 | 1162 | 8 | AF134200 Labeo roh |
| 11 | 324.4 | 39.6 | 603 | 8 | PNAGH M63713 Pangasius p |

12 324.4 39.6 1176 8 PGSGHA
 13 313.2 38.2 1132 8 AF147792
 14 284 34.7 633 10 E02632
 15 282.8 34.5 742 8 CAGHG
 16 280.2 34.2 633 10 E02630
 17 280.2 34.2 1120 8 OKGHI
 18 280.2 34.2 1176 8 OMMSGH
 19 280.2 34.2 1176 10 E04473
 20 279.2 34.1 567 10 E02633
 21 278.6 34.0 633 10 E00637
 22 278.6 34.0 633 10 E00815
 23 278.6 34.0 633 10 E00819
 24 278.6 34.0 633 10 E01236
 25 278.6 34.0 633 10 E01334
 26 278.6 34.0 633 10 I01407
 27 278.6 34.0 891 10 E02682
 28 278.6 34.0 1120 8 ONHGHSA
 29 278.6 34.0 1201 8 ONHGHCOHO
 30 278.6 34.0 1201 10 I68306
 31 278.2 34.0 1212 8 SMOGHTC
 32 277.6 33.9 1169 8 SSMGHTC
 33 277 33.8 633 10 E02631
 34 277 33.8 634 56 SYNGHSMHEC
 35 277 33.8 1171 8 SMOGHTA
 36 275.4 33.6 1161 8 SMOGHI
 37 275 33.6 633 10 E00964
 38 275 33.6 633 10 E05294
 39 275 33.6 633 10 E05652
 40 275 33.6 633 10 I01409
 41 275 33.6 1159 8 SMOGH2
 42 275 33.6 1180 8 OKGHI
 43 273.8 33.4 1138 8 S50867
 44 263.6 32.2 1228 8 S66470
 45 248.4 30.3 2838 8 CCGHG

ALIGNMENTS

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 LOCUS Cyprinus carpio growth hormone (GH) mRNA, complete cds.
 DEFINITION M27000
 ACCESSION M27000.1 GI:529027
 VERSION growth hormone.
 KEYWORDS Cyprinus carpio pituitary gland cDNA to mRNA.
 ORGANISM Cyprinus carpio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 1 (bases 1 to 1164)
 TITLE Koen, Y., Sarid, S., Ber, R. and Daniel, V.
 JOURNAL Carp growth hormone: molecular cloning and sequencing of cDNA
 MEDLINE Gene 77, 309-315 (1989)
 COMMENT 89326147
 FEATURES On Aug 9, 1994 this sequence version replaced gi:341578.
 Location/Qualifiers
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 37..1147
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 37..102
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 Best Local Similarity 100.0%; Pred. No. 6.6e-146;
 Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 103 TCAGACAAACCGCGCTCTTCAATATGAGTATGAGGACAGCGCTTGCCTGAGGAACGACAGAGCTG 162
 QY 313 GCTGCAAAATGATTAACGACTTTGAGGACAGCGCTTGCCTGAGGAACGACAGAGCTG 372
 DB 163 GCTGCAAAATGATTAACGACTTTGAGGACAGCGCTTGCCTGAGGAACGACAGAGCTG 222
 QY 373 AGTAAATCTTCCCTCTGCTTCTGCAATTTGACTACATTGAGGCGGCTGCTGGAAGA 432
 DB 223 AGTAAATCTTCCCTCTGCTTCTGCAATTTGACTACATTGAGGCGGCTGCTGGAAGA 282
 QY 433 GATGAACACAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTTCACCTCATTTGAG 492
 DB 283 GATGAACACAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTTCACCTCATTTGAG 342
 QY 493 TCCTGGGAGTCCCAAGCCAGTCCCTGAGCGGAACCGCTCTCAAAACAGCGCTGACCGTAGGG 552
 DB 343 TCCTGGGAGTCCCAAGCCAGTCCCTGAGCGGAACCGCTCTCAAAACAGCGCTGACCGTAGGG 402
 QY 553 AACCCCAACCGCTCAGTGAAGCTGGCGGAGCTTGAATGGGATCGATGCTGCTCATC 612
 DB 403 AACCCCAACCGCTCAGTGAAGCTGGCGGAGCTTGAATGGGATCGATGCTGCTCATC 462
 QY 613 CAGGATGCTCGATGGTCAACCAACATGATGATAAGCACTCTTGGCGCTGCCTTTT 672
 DB 463 CAGGATGCTCGATGGTCAACCAACATGATGATAAGCACTCTTGGCGCTGCCTTTT 522
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 DB 523 GAGGATCTTACTTGACCATGGGGAGAACACCTCAGAGAGCTTTTCTGCTGCTGGCT 582
 QY 733 TCCTTCAAGAAGGACATGCACAAAGTCGAGACCTACTTGAAGGTTGCAATTCAGAGAGA 792
 DB 583 TCCTTCAAGAAGGACATGCACAAAGTCGAGACCTACTTGAAGGTTGCAATTCAGAGAGA 642
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 ACCESSION AF069398
 VERSION AF069398.1 GI:3202014
 KEYWORDS goldfish.
 SOURCE Carassius auratus
 ORGANISM Carassius auratus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Cyprininae; Carassius.
 1 (bases 1 to 1117)
 REFERENCE Law, M.S., Cheng, K.W., Fung, T.K., Chan, Y.H., Yu, K.L. and Chan, K.M.

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|------------|---|----------|-------------|
| CCGH | 1158 bp | mRNA | 22-MAR-1995 |
| LOCUS | | | |
| DEFINITION | Cyprinus carpio mRNA for growth hormone. | | |
| ACCESSION | X13670 | | |
| VERSION | X13670.1 | GI:62607 | |
| KEYWORDS | growth hormone. | | |
| SOURCE | common carp. | | |
| ORGANISM | Cyprinus carpio | | |
| | Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; | | |
| | Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; | | |
| | Cyprinoidae; Cyprinidae; Cyprininae; Cyprinus. | | |
| REFERENCE | 1 (bases 1 to 1158) | | |
| AUTHORS | Chang, W.C. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (28-NOV-1988) Chang W.C., Institute of Biological | | |
| | Chemistry, Academia Sinica, PO Box 23-106, Taipei, Taiwan, ROC | | |
| REFERENCE | 2 (bases 1 to 1158) | | |
| AUTHORS | Chao, S.C., Pan, F.M. and Chang, W.C. | | |
| TITLE | Purification of carp growth hormone and cloning of the | | |
| | complementary DNA | | |
| JOURNAL | Biochim. Biophys. Acta 1007 (2), 233-236 (1989) | | |
| MEDLINE | 89150258 | | |
| FEATURES | Location/Qualifiers | | |
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Best Local Similarity 95.6%; Pred. No. 7.5e-135;
Matches 542; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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| Db | 287 | GATGAACACAGAGAGAGCTCTATGTTTGAAGCTCTCTTGGCATTTCCTTCCGCTCATTTGAG | 346 |
| Qy | 493 | TCCTGGGAGTTTCCCAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGACCTGACCGTAGGG | 552 |
| Db | 347 | TCTTGGGAGTACCCACGCCAGACCCCTGAGCGGGAACCGTCTCAACAGCCTGACCGCGGG | 406 |
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| Db | 407 | AACCCCAACAGGATCACTGAGAAGCTGCGCGGACCTTGAAAAATGGGCATCAATGTGCTCAT | 466 |
| Qy | 613 | CAGGCATGTCGATGTCAACCAACATGGATGATTAACGACTTCCCTGCGCGCTGCCTTTT | 672 |
| Db | 467 | AAGGGAAGTCTCGATGTCAACCAACATAGATGATTAACGACTTCCCTTACCACCTGCCTTTT | 526 |
| Qy | 673 | GAGGACTTCTACTTGTGACCATGCGGGGAGAACAACTCAGAGAGAGCTTTCGCTCTGCTGGCT | 732 |
| Db | 527 | GAGGACTTCTACTTGTGACCATGCGGGGAGAACAACTCAGAGAGAGCTTTCGCTCTGCTGGCT | 586 |
| Qy | 733 | TGCTTCAAGAGGACATGCAACAAGTCGAGACCTTACTTGAGGGTTGCAAAATTCAGAGAGA | 792 |
| Db | 587 | TGTTTTAAGAGGACATGCAACAAGTCGAAACCTTACCTGAGGGTTGCAAAATTCAGAGAGA | 646 |
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| HNPGH | | HNPGH | |
| LOCUS | | H.nobilis (Bighead carp) mRNA for growth hormone. | VRT 29-DEC-1993 |
| DEFINITION | | X60473.1 GI:65313 | |
| ACCESSION | | X60473.1 | |
| VERSION | | X60473.1 | |
| KEYWORDS | | growth hormone. | |
| SOURCE | | noble carp. | |
| ORGANISM | | Hypophthalmichthys nobilis | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; | |
| AUTHORS | | Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; | |
| JOURNAL | | Cyprinidae; Cyprinidae; Leuciscinae; Hypophthalmichthys. | |
| REFERENCE | | 1 (bases 1 to 1158) | |
| AUTHORS | | Huang, F.I. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Submitted (09-JUL-1991) F.L. Huang, Institute of Biological | |
| REFERENCE | | Chemistry, Academia Sinica, P O Box 23-106, Taipei, Taiwan | |
| AUTHORS | | 2 (bases 1 to 1158) | |
| TITLE | | Chang, Y.S., Liu, C.S., Huang, F.L. and Lo, T.B. | |
| JOURNAL | | The primary structures of growth hormones of three cyprinid | |
| MEDLINE | | species: bighead carp, silver carp, and grass carp | |
| FEATURES | | Gen. Comp. Endocrinol. 87 (3), 385-393 (1992) | |
| source | | 93051159 | |
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Best Local Similarity 92.08; Pred. No. 4.7e-128;
Matches 527; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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DB 94 CTCAGAGAACAGCGGCTTTCAACACGACGATCCTCGGTGTTCAACACCTGCACACGCT 153

QY 312 GGCTGCAAAATGATTAAACGACTTTGAGGACAGCCTGTTGCCTGAGGAACGACACAGCT 371
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DB 154 GGCTGCAAAATGATTAAACGACTTTGAGGACAACTGTTGCCTGAGGAACGACACAGCT 213

QY 372 GAGTAAATCTCCCTCTGCTCTTCTGCAATTCGACTACATGAGGCGGCTGCTGGAAA 431
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DB 214 GAGTAAATCTTTCCTCTGCTCTTTCGCAACTCTGACTCCATTGAGCGGCCACCTGGAAA 273

QY 432 AGATGAACACAGAAAGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTCACTTCATTGA 491
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DB 274 AGATGAACGAGAAAGAGCTCTATGTTGAGCTCCTTCGCATCTCTTTCGCCCTCATGA 333

QY 492 GTCTGGGAGTTCCCAAGCCAGTCCCTTGAGCGGAACCGTCTCAAAACAGCTGACCGTAGG 551
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DB 334 GTCTGGGAGTTCCCAAGCCAGACCCCTGAGCGGAGCGCTCTCAAAACAGCTTGACCGTCGG 393

QY 552 GAACCCCAACGACTCACTCAGAGCTGCGCGACTTCAAAATGGGCATCAGTGTGCTCAT 611
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DB 394 GAACCCCAACGACTCACTCAGAGCTGCGCGACTTCAAAATGGGCATCAGCGTGTGCTCAT 453

QY 612 CCAGGCATGTCTCATGGTCAACCAACATCGATGATTAAGCACTCTTCGCGCTGCCCTTT 671
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DB 454 CAAGGGATGCTGGATGGTCAACCAACATGGATGATTAAGCACTCCCTGCCGCTGCCCTTT 513

QY 672 TGAGGACTTCTACTTGACCATGGGGGAGACAACCTCAGAGAGAGCTTTGCTGTGCTGGC 731
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DB 514 TGAGGATTTCTACTTGACCATGGGGGAGAGCAGCCTCAGAGAGAGCTTCGCTGCTTCTTGC 573

QY 732 TTGCTTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAATTTGCAGGAG 791
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DB 574 TTGCTTCAAGAGGACATGCACAAAGTGGAAACTTACCTAAGGGTTGCAATTTGCAGGAG 633

QY 792 ATCCCTGGATTCCAACTGCACCCCTGTAG 819
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RESULT      7
CAU28388
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CAU28388      567 bp      mRNA      VRT      29-OCT-1996
Carassius auratus growth hormone mRNA, partial cds.
U28388
GI:1143868
goldfish.
Carassius auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Carassius.
1. (bases 1 to 567)

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AUTHORS Mahmoud, S.S., Moloney, M.M. and Habibi, H.R.
 TITLE Cloning and sequencing of the goldfish growth hormone cDNA
 JOURNAL Gen. Comp. Endocrinol. 101 (2), 139-144 (1996)
 MEDLINE 96271507
 REFERENCE 2 (bases 1 to 567)
 AUTHORS Mahmaoud, S.S.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUN-1995) Scheil S. Mahmaoud, Biological Sciences,
 University of Calgary, 2500 University Drive NW, Calgary, AB, T2N
 1N4, Canada

FEATURES
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 BASE COUNT 152 a 149 c 135 g 131 t
 ORIGIN

Query Match 61.2%; Score 501.4; DB 8; Length 567;
 Best Local Similarity 92.8%; Pred. No. 8.6e-128;
 Matches 526; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 253 TCAGAACACGAGCGCTCTCAATAATGCACTCATCTGTTACACACCTGCACAGCTG 312
 DB 1 TCCGAGAACGAGCGCTCTTCCACCAACGAGTCATCTGTTACACGCTGCACAGCTG 60

QY 313 GCTGCAAAATGATTAAAGCACTTTGAGGACAGCCCTGTTGCCCTGAGGAACGACAGAGCTG 372
 DB 61 GCCGCTAAATGATTAAAGCACTTTGAGGACAGCCCTGTTGCCCTGAGGAGCGCAGAGCTG 120

QY 373 AGTAAATCTTCCCTCTCTCTTTCTGCAATCTGACTACATTTGAGGCGCTGCTGGAAA 432
 DB 121 AGTAAATCTTCCCTCTCTCTTTCTGCAATCTGACTACATTTGAGGCGCCACTGGAAA 180

QY 433 GATGAACACAGAGAGCTCATGCTGAAGCTTCTTCGCATCTCTTTTCACTCATTTAG 492
 DB 181 GATGAACACAGAGAGCTCATGTTGAAGCTTCTTCGCATTTCTTCCGCTCATTTAG 240

QY 493 TCCTGGGAGTCCCAAGCCAGTCCCTGAGCGAAGCCGCTCAACAGCCCTGACCGTAGG 552
 DB 241 TCTTGGGAGTACCCAGTCAAGCCCTGAGTGAACCGCTCAACAGCTGATCGTAGG 300

QY 553 AACCCCAACGAGCTCACTGAGAGCTGGCCGACTTTGAAAATGGGCATCAGTGTCTCATC 612
 DB 301 AACCCCAACGAGCTCACTGAGAGCTGGCCGACTTTGAAAATGGGCATCAATGTCTCAT 360

QY 613 CAGGATCTCTGATGTTCAACCAACATGATGATACGACTCTCTGCGCTGCCTTTT 672
 DB 361 AAGGAGTCTCGATGTTCAACCAACATGATGATACGACTCTCTGCGCTGCCTTTT 420

QY 673 GAGGATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 732
 DB 421 GAGGATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 480

QY 733 TGCTTCAAGAGGAGGATGCAACAACTCGAGACCTACTTTGAGGTTGCAAAATTCAGAGGA 792
 DB 481 TGTTTAAAGAGGAGGATGCAACAACTCGAGACCTACTTTGAGGTTGCAAAATTCAGAGGA 540

QY 793 TCCCTGGATTCCAACTGCACCCCTGTAG 819
 DB 541 TCCCTGGATTCCAACTGCACCCCTGTAG 567

RESULT 8

CIPGH 1171 bp mRNA VRT 14-JUN-1994
 LOCUS C idellus (Grass carp) mRNA for growth hormone.
 DEFINITION X60474
 ACCESSION X60474.1 GI:62710
 VERSION growth hormone.
 KEYWORDS growth hormone.
 SOURCE grass carp.
 ORGANISM Ctenopharyngodon idella
 Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
 Neopterygii; Teleostei; Euteleostei; Osteichthyes; Cypriniformes;
 Cyprinidae; Cyprinidae; Cyprinidae; Cyprinidae; Ctenopharyngodon.
 1 (bases 1 to 1171)
 Huang, F.I.
 Direct Submission
 Submitted (09-JUL-1991) F.L. Huang, Institute of Biological
 Chemistry, Academia Sinica, P O Box 23-106, Taipei, Taiwan
 2 (bases 1 to 1171)
 Chang, Y.S., Huang, F.I. and Lo, T.B.
 The cDNA and primary structure of pregrowth hormones of three
 species of Cyprinidae: silver carp, bighead carp and grass carp
 Unpublished
 Location/Qualifiers
 1..1171
 /organism="Ctenopharyngodon idella"
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 KWINDFEDNLPEERRQLSKIPFLSCNDSIEAPTKDETKSSMLKLLRISFRLE
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 BASE COUNT 320 a 267 c 256 g 328 t
 ORIGIN

Query Match 61.1%; Score 500.8; DB 8; Length 1171;
 Best Local Similarity 92.6%; Pred. No. 1.3e-127;
 Matches 526; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 252 CTCAGAACACGAGCGCTCTTCAATAATGCACTCATCTGTTACACACCTGCACAGCT 311
 DB 89 CTCAGAACACGAGCGCTTTTCAACACGAGTCATCCGTTTCAACACCTGCACAGCT 148

QY 312 GGTGCAAAATGATTAAAGCACTTTGAGGACAGCTTTCCTGCTGAGGAGGAGCAGAGCT 371
 DB 149 GGTGCAAAATGATTAAAGCACTTTGAGGACAGCTTTCCTGCTGAGGAGGAGCAGAGCT 208

QY 372 GAGTAAATCTTCCCTCTGCTTTCTGCAATCTGACTACATTTGAGGCGCTGCTGGAAA 431
 DB 209 GAGTAAATCTTCCCTCTGCTTTCTGCAATCTGACTACATTTGAGGCGCTGCTGGAAA 268

QY 432 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTTCGCATCTCTTTTCACTCATTTGA 491
 DB 269 AGATGAACACAGAGAGCTCTATGTTGAAGCTTCTTTCGCATCTCTTTTCCGCTCATTTGA 328

QY 492 GTCTTGGGAGTTTCCCAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGCGTGCAGCTAGG 551
 DB 329 GTCTTGGGAGTTTCCCAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGCGTGCAGCTAGG 388

QY 552 GAACCCCAACAGCTCACTCAGAGCTGCCGAGCTTCAAAATGGCATGCTGCTCAT 611
 DB 389 GAACCCCAACAGCTCACTCAGAGCTGCCGAGCTTCAAAATGGCATGCTGCTCAT 448

QY 612 CCAGGATCTGCTGATGGTCAACCAACATGGATGATGAACAGCTCTTTCGCGCTGCCTTT 671
 DB 449 CAAGGATCTGCTGATGGTCAACCAACATGGATGATGAACAGCTCTTTCGCGCTGCCTTT 508

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QY 672 TGAGGACTTCTACTTACCATTGGGAGAACAACTCAGAGAGAGCTTTCTGCTGCGG 731
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Db 509 TGAGGATTCTTACTTAACTATGGGAGAGACCCCTCAGAGAGAGCTTTCTGCTGCGG 568
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Db 569 TTGCTTTCAAGAGGAGCATGCACAAAGTCGAGAACTTACCTAAGGGTTGCAAAATTCGAGGAG 628
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QY 792 ATCCCTGGATTCCAACTGCACCTGTAG 819
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Db 629 ATCCCTGGATTCAAACTGCACCTGTAG 656
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RESULT 9
CTEGRH CTEGRH 1171 bp mRNA VRT 03-JAN-1995
LOCUS Ctenopharyngodon idella growth hormone mRNA, complete cds.
DEFINITION M27094
ACCESSION M27094
VERSION M27094.1 GI:609443
KEYWORDS growth hormone.
SOURCE Ctenopharyngodon idella pituitary gland cDNA to mRNA.
ORGANISM Ctenopharyngodon idella
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Ctenopharyngodon.
REFERENCE 1 (bases 1 to 1171)
AUTHORS Ho,W.K., Tsang,W.H. and Dias,N.P.
TITLE Cloning of the grass carp growth hormone cDNA
JOURNAL Biochem. Biophys. Res. Commun. 161 (3), 1239-1243 (1989)
MEDLINE 89302103
COMMENT On Jan 4, 1995 this sequence version replaced gi:341636.
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                    PFEDFYLTMGESSLRESPLACFKKDMHKVETYLVRVANCRRSLDSNCTL"
sig_peptide 44..100
mat_peptide 101..670
polyA_signal 1154..1159
BASE COUNT 313 a 270 c 259 g 329 t
ORIGIN

Query Match 60.6%; Score 496; DB 8; Length 1171;
Best Local Similarity 92.1%; Pred. No. 2.8e-126;
Matches 523; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 252 CTCAGACACACCGCGCTCTCAATAATGACGTCATTCGTGTACACACACCTGCACCGCT 311
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Db 109 CTCAGACACACCGCGCTCTTCAACACCGCAGTCATACGTTTCAACACCTGCACCGCT 168
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QY 312 GCCTCAAAATGATTAACTTTGAGGACAGCGCTGTTCCTCGTGAGACGACGACAGCT 371
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Db 169 GCCTCAAAATGATTAACTTTGAGGACAGCGCTGTTCCTCGTGAGACGACGACAGCT 228
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QY 372 GAGTAAATCTTCCCTCTCTCTTCTGCAATCTGTGACTACATTCAGCGCGCTGCTGAAA 431
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Db 229 GAGTAAATCTTCCCTCTCTCTTCTGCAATCTGTGACTCAATTTGAGGCGCCCACTGAAA 288
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QY 432 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCACCTCATTTGA 491
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Db 289 AGATGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCGCTCATTTGA 348
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QY 492 GTCCCTGGAGTTCCCAAGCCAGTCCCTCAGCGGACCCCTCTCAACACGCTACCGTAG 551
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Db 349 GTCCCTGGAGTTCCCAAGCCAGTCCCTCAGCGGACCCCTCTCAACACGCTACCGTAG 408
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QY 552 GAACCCCAACAGCTCACTGAGAAAGCTGGCCGACTTGAATAATGGGCATCAGTGTGCTCAT 611
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Db 409 GAACCCCAACAGCTCACTGAGAAAGCTGGCCGACTTGAATAATGGGCATCAGTGTGCTCAT 468
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QY 612 CCAGGCATGCTCATGCTCAACCAACATGATGATTAACGACTCCTTGGCCCTGCTTT 671
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Db 469 CAAGGGATGCTGATGCTCAACCAACATGATGATTAACGACTCCTTGGCCCTGCTTT 528
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QY 672 TGAGGACTTCTACTTACCATTGGGAGAACAACTCAGAGAGAGCTTTCTGCTGCTGCG 731
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QY 732 TTGCTTCAAGAGGAGCATGCACAAAGTCGAGACCTACTTCTGAGGGTTGCAAAATTCGAGGAG 791
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QY 792 ATCCCTGGATTCCAACTGCACCTGTAG 819
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Db 649 ATCCCTGGATTCCAACTGCACCTGTAG 676
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RESULT 10
AF134200 AF134200 1162 bp mRNA VRT 17-MAY-1999
LOCUS Labeo rohita growth hormone precursor, mRNA, complete cds.
DEFINITION AF134200
ACCESSION AF134200
VERSION AF134200.1 GI:4836724
KEYWORDS
SOURCE Labeo rohita.
ORGANISM Labeo rohita
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Labeo.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Venugopal,T., Pandian,T.J. and Mathavan,S.
TITLE Labeo rohita (Indian major carp) growth hormone cDNA, complete cds
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1162)
AUTHORS Venugopal,T., Pandian,T.J. and Mathavan,S.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-1999), Department of Genetics, Madurai Kamara]
University, School of Biological Sciences, Madurai, TN 625 021,
India
FEATURES
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mat_peptide 115..669
polyA_signal 1140..1145
polyA_site 1162
BASE COUNT 321 a 256 c 249 g 336 t
ORIGIN

Query Match 56.2%; Score 460.6; DB 8; Length 1162;
Best Local Similarity 89.8%; Pred. No. 1.7e-116;
Matches 509; Conservative 0; Mismatches 49; Indels 9; Gaps 1;

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ACCESSION L27835
 VERSION L27835.1 GI:450294
 KEYWORDS growth hormone.
 SOURCE Pangasianodon gigas cDNA to mRNA.
 ORGANISM Pangasianodon gigas
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Siluriformes; Pangasiidae; Pangasianodon.
 REFERENCE 1 (bases 1 to 1176)
 AUTHORS Lemaire, C., Warit, S. and Panyim, S.
 TITLE Giant catfish Pangasianodon gigas growth hormone-encoding cDNA: cloning and sequencing by one-sided polymerase chain reaction
 JOURNAL Gene 149 (2), 271-276 (1994)
 MEDLINE 95047487
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 Location/Qualifiers
 1..1176
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 Db 128 GAGAACCGGGCTCTTCAACACCGAGTCTCGTGTGCAACACCTTCATCAGCTGGT 187
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 QY 316 GCAAAATGATTACGACTTTGAGGACGCTGTGCTGAGNACCGACACCTCAGT 375
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 Db 188 GCAGATGATGATGACTTTGAGGAGCTGTGTACCTGAAGAACCAACACGCTGAGC 247
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 QY 376 AAAATCTTCCTGTCTTCTGCAATTCGACTACATCAGGCGGCTGTGGAAAAAGAT 435
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 Db 248 AGATTTTCCCTGTCTTCTGCACTCGGACTCCATCGAGCTCTCGCAGGCAAGAC 307
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 QY 436 GAAACACAGAAGAGCTCTATGCTGAAGCTTCTTCGCTATCTCTTTACCTCATTGAGTCC 495
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 Db 308 GAGACCCAGAAGAGCTGTGTGTAATTCGTCACACCTCTTACCGTCTGATCGAGTCG 367
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 QY 496 TGGGAGTTCCCAAGCCAGTCCCTTGAGCGGAACCGCTTCAACACCGCTGACCGTAGGGAAC 555
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 Db 368 TGGGAGTTCC-----CAGCAAGAAGCTCGGCAAC 397
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 QY 556 CCCAACCACTCACTGAGAGCTGGCGGACTTGAATGGGCATCAGTGTGCTCATCCAG 615
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Db 398 CCCAACCACTCTCAGAGAAGCTGGCTGACCTGAAATGGGCATCGGCTGCTTATCGAG 457
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 QY 676 GACTTCTACTTGGACCATGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGCTGCTGC 735
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 Db 578 TTCAAGAGGACATGCACAAAGTCGAGACCTTATCTCAGCGTGGCCAAGTGCAGGAGATCC 637
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 QY 796 CTGGATTCCAACTGCACCTGTAG 819
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 Db 638 CTGGATTCCAACTGCACCTGTAG 661
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 RESULT 13
 AF147792 1132 bp mRNA VRT 30-MAY-1999
 LOCUS AF147792 Heteropneustes fossilis growth hormone (GH) mRNA, complete cds.
 DEFINITION Heteropneustes fossilis growth hormone (GH) mRNA, complete cds.
 ACCESSION AF147792
 VERSION AF147792.1 GI:4927275
 KEYWORDS Heteropneustes fossilis.
 SOURCE Heteropneustes fossilis.
 ORGANISM Heteropneustes fossilis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Siluriformes; Siluridae; Heteropneustes.
 REFERENCE 1 (bases 1 to 1132)
 AUTHORS Anathy, V., Pandian, T.J. and Mathavan, S.
 TITLE Heteropneustes fossilis growth hormone mRNA
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1132)
 AUTHORS Anathy, V., Pandian, T.J. and Mathavan, S.
 TITLE Direct Submission
 JOURNAL Submitted (02-MAY-1999) Genetics, Madurai Kamaraj University,
 School of Biological Sciences, Madurai, TN 625 021, India
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 59..661
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 Best Local Similarity 74.6%; Pred. No. 9.2e-76;
 Matches 421; Conservative 0; Mismatches 113; Indels 30; Gaps 1;
 QY 256 GACAACCGGGCTCTTCAATATGCGTATCGGTACACACCTGCACCGCTGGCT 315

AUTHORS Trofimova, I.N.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1994) I.N. Trofimova, Limnological Institute,
Irkutsk 664033, PO Box 4199, Russia, USSR
FEATURES Location/Qualifiers
Source 1. .742
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sig_peptide 39. .104
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gene 39. .671
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BASE COUNT 200 a 192 c 186 g 164 t
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Query Match 34.5%; Score 282.8; DB 8; Length 742;
Best Local Similarity 71.2%; Pred. No. 2.3e-67;
Matches 406; Conservative 0; Mismatches 152; Indels 12; Gaps 2;
QY 256 GAAACACAGCGGCTCTTAATAATGAGTCATTGCGTGTACAAACACCTGCACACGCTGGCT 315
DB 108 GAAACACAGCGGCTCTTAACATCGCAGTCACACCGGTGCAACATCTCCACCTAATGGCT 167
QY 316 GCATAAATGATTACGACCTTTAGGACAGCCTGTTGCTGAGGAACGACAGACGCTGAGT 375
DB 168 CAGAAAATGTTCAATGACCTTGAAGCACCCCTGTTGCTGATGAACGACAGACGCTGAAC 227
QY 376 AAAATCTCCCTCTGCTTCTTCAATTCGACTATGACGAGCGGCTGCTGAAAAGAT 435
DB 228 AAGATATTCTGCTGACCTCTGTAATCTGACTCCATGCTGAGCCCAATTGACAAGCTT 287
QY 436 GAAACACAGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTTCACCTCATTTGAGTCC 495
DB 288 GAGACTCAGAGAGTTCAGTCTGAAAGCTGCTCCATATCTCTTCGCTGATTTGAATCA 347
QY 496 TGGGAGTTCCCAAGCCAGTCCCTGAGCGGAACCGTCTCAAAACAGCCTGACCGTAGGGAAC 555
DB 348 TGGGAGTACCTTAGCCAGACCCCTG-----ACCATCTCCAAAGTCTAATGGTCAGAAAC 401
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QY 616 GCATGCTCGATGTTCAACCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 675
DB 462 GGGAGCCAGATGGCGCTACTAAGCCTGGATGACAATGACTTTTCAGCAGCTGCCCCCCTAC 521
QY 676 GACTTCTACTTGACCA-----TGGGGGAGACAAACCTCAGAGAGAGCTTTTCGCTGCTG 729
DB 522 GGAAACTACTACCAAGACCTGGGGGGCGGCGCAACGTCAGGAGGAACTACGAGCTGTTG 581
QY 730 GTTGTCTCAAGAGGACATGACAAAGTCGAGACCTACTTTAGGGGTGCAAAATTCAGG 789
DB 582 GCCTGCTTCAAGAGGACATGACAAAGTCGAGACCTACTTGACCGTTGCCAAGTCGAGG 641
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Db 642 AAGTCACTGGAGGCCAACTGCACCTCTGTAG 671
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OM nucleic - nucleic search, using sw model

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Title: US-09-402-488a-3

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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*

1: /SID56/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /SID56/gcgdata/geneseq/geneseq/NA1985.DAT.*
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8: /SID56/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT.*
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11: /SID56/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /SID56/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /SID56/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /SID56/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /SID56/gcgdata/geneseq/geneseq/NA1995.DAT.*
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18: /SID56/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /SID56/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /SID56/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID56/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|-------|-------------|----------------|--------------------|
| 1 | 819 | 100.0 | 20 V83967 | DNA encoding His-c |
| 2 | 452.8 | 55.3 | 670 21 288227 | Misgurnus mizolepi |
| 3 | 280.2 | 34.2 | 891 10 N91667 | Salmon growth horm |
| 4 | 278.6 | 34.0 | 633 7 N60341 | Sequence encoding |
| 5 | 278.6 | 34.0 | 1176 14 Q38832 | Pre-growth hormone |
| 6 | 278.6 | 34.0 | 1201 16 Q98905 | Coho Salmon growth |
| 7 | 277.6 | 33.9 | 633 11 Q06417 | Sequence encoding |
| 8 | 277 | 33.8 | 633 7 N60340 | Sequence encoding |
| 9 | 275.6 | 33.7 | 564 8 N70829 | DNA encoding fish |
| 10 | 275.4 | 33.6 | 1119 13 Q29359 | Salmon growth horm |
| 11 | 273.8 | 33.4 | 633 11 Q06132 | Sequence encoding |

| | | | | |
|----|-------|------|----------------|---------------------|
| 12 | 270.6 | 33.0 | 633 11 Q06131 | Sequence encoding |
| 13 | 217 | 26.5 | 555 12 Q10874 | Plasmid pMWTfw1 co |
| 14 | 203.2 | 24.8 | 630 8 N70544 | Eel growth hormone |
| 15 | 203.2 | 24.8 | 630 9 N81504 | cDNA encoding GH-1 |
| 16 | 183.8 | 22.4 | 564 9 N80701 | Sequence encoding |
| 17 | 169.4 | 20.7 | 887 11 Q06743 | Insert from ptIGH6 |
| 18 | 167.8 | 20.5 | 887 11 Q05160 | Fragment of plasmid |
| 19 | 167 | 20.4 | 5108 21 288226 | Misgurnus mizolepi |
| 20 | 166.4 | 20.3 | 337 14 Q36414 | Plasmid PSGHE1 fra |
| 21 | 166.4 | 20.3 | 381 14 Q36415 | Plasmid PSGHEC-1 f |
| 22 | 166.4 | 20.3 | 414 14 Q36422 | Plasmid PSGHEC-14B |
| 23 | 166.4 | 20.3 | 429 12 Q14067 | HCV detecting pept |
| 24 | 166.4 | 20.3 | 429 14 Q36416 | Plasmid PSGHEC-14 |
| 25 | 166.4 | 20.3 | 429 14 Q36421 | Plasmid PSGHEC-14A |
| 26 | 166.4 | 20.3 | 516 14 Q36417 | Plasmid PSGHEC-18 |
| 27 | 166.4 | 20.3 | 537 12 Q14066 | HCV detecting pept |
| 28 | 166.4 | 20.3 | 537 14 Q36418 | Plasmid PSGHEC-141 |
| 29 | 166.2 | 20.3 | 942 10 N90111 | Fish growth hormon |
| 30 | 164.8 | 20.1 | 337 12 Q14062 | HCV detecting pept |
| 31 | 164.8 | 20.1 | 381 12 Q14063 | HCV detecting pept |
| 32 | 164.6 | 20.1 | 944 12 Q10912 | Fish growth hormon |
| 33 | 163.2 | 19.9 | 414 12 Q14068 | HCV detecting pept |
| 34 | 161.6 | 19.7 | 429 12 Q14064 | HCV detecting pept |
| 35 | 157.2 | 19.2 | 576 9 N81780 | Sequence of synthe |
| 36 | 156.8 | 19.1 | 516 12 Q14065 | HCV detecting pept |
| 37 | 156.2 | 19.1 | 576 4 N30046 | Sequence of synthe |
| 38 | 154 | 18.8 | 714 21 A54214 | Synthetic construc |
| 39 | 153.2 | 18.7 | 608 10 N90364 | Fish growth hormon |
| 40 | 152.4 | 18.6 | 576 9 N80724 | Cattle somatotropi |
| 41 | 152.4 | 18.6 | 601 11 Q05662 | EK-bovine growth h |
| 42 | 152.4 | 18.6 | 601 12 Q10188 | EK-bovine growth h |
| 43 | 152.4 | 18.6 | 601 14 Q38308 | Plasmid EK-bGH. S |
| 44 | 152.4 | 18.6 | 601 14 Q42407 | Bovine growth Horm |
| 45 | 152.4 | 18.6 | 601 14 Q43934 | EK-BGH (Metpheprol |

ALIGNMENTS

RESULT 1
V83967
ID V83967 standard; DNA; 819 BP.
XX
AC V83967;
XX
DT 09-MAR-1999 (first entry)
XX
DNA encoding His-chymosin pro-peptide-carp growth hormone.
DE
XX
Fusion protein; bovine chymosin pro-peptide; leech hirudin;
KW antioagulant protein; autocatalytically maturing zymogen;
KW carp growth hormone; vaccine; ss.
XX
XX Synthetic.
OS Bos sp.
OS Cyprinus carpio.
XX
FH Key Location/Qualifiers
FT CDS 1..819
FT FT /tag= a
FT FT /product= His-chymosin_pro-peptide-carp_growth_hormone
FT FT /tag= b
FT FT /tag= c
FT FT /note= "encodes bovine chymosin pro-peptide"
FT FT /tag= c
FT FT /note= "carp growth hormone"
XX
XX WO9849326-A1.
XX
XX 05-NOV-1998.
XX
XX 23-APR-1998; 98WO-CA00398.


```
FT      /tag= b
FT      /note="portion filled in by klenow fragment"
```

11

Figure 2

1. *What is the purpose of this study?*
 2. *What are the research objectives?*
 3. *What is the research methodology?*
 4. *What are the results of the study?*
 5. *What are the conclusions of the study?*
 6. *What are the limitations of the study?*
 7. *What are the implications of the study?*
 8. *What are the future research directions?*
 9. *What are the contributions of the study?*
 10. *What are the key findings of the study?*
 11. *What are the main results of the study?*
 12. *What are the primary outcomes of the study?*
 13. *What are the secondary outcomes of the study?*
 14. *What are the tertiary outcomes of the study?*
 15. *What are the quaternary outcomes of the study?*
 16. *What are the quinary outcomes of the study?*
 17. *What are the senary outcomes of the study?*
 18. *What are the septenary outcomes of the study?*
 19. *What are the octenary outcomes of the study?*
 20. *What are the nonary outcomes of the study?*
 21. *What are the decenary outcomes of the study?*
 22. *What are the undecenary outcomes of the study?*
 23. *What are the duodecenary outcomes of the study?*
 24. *What are the tredecenary outcomes of the study?*
 25. *What are the quattuordecenary outcomes of the study?*
 26. *What are the quindecenary outcomes of the study?*
 27. *What are the sexdecenary outcomes of the study?*
 28. *What are the septendecenary outcomes of the study?*
 29. *What are the octodecenary outcomes of the study?*
 30. *What are the nonodecenary outcomes of the study?*
 31. *What are the vigintenary outcomes of the study?*
 32. *What are the unvigintenary outcomes of the study?*
 33. *What are the bivigintenary outcomes of the study?*
 34. *What are the trivigintenary outcomes of the study?*
 35. *What are the quadvigintenary outcomes of the study?*
 36. *What are the quinvigintenary outcomes of the study?*
 37. *What are the sexvigintenary outcomes of the study?*
 38. *What are the septenvigintenary outcomes of the study?*
 39. *What are the octovigintenary outcomes of the study?*
 40. *What are the nonavigintenary outcomes of the study?*
 41. *What are the vigintigintenary outcomes of the study?*
 42. *What are the untrigintenary outcomes of the study?*
 43. *What are the bistrigintenary outcomes of the study?*
 44. *What are the tristrigintenary outcomes of the study?*
 45. *What are the quadrigintenary outcomes of the study?*
 46. *What are the quingrigintenary outcomes of the study?*
 47. *What are the sextrigintenary outcomes of the study?*
 48. *What are the septetrigintenary outcomes of the study?*
 49. *What are the octetrigintenary outcomes of the study?*
 50. *What are the nonetrigintenary outcomes of the study?*
 51. *What are the trigintigintenary outcomes of the study?*
 52. *What are the unquadrigintenary outcomes of the study?*
 53. *What are the biquadrigintenary outcomes of the study?*
 54. *What are the triquadrigintenary outcomes of the study?*
 55. *What are the quadragintenary outcomes of the study?*
 56. *What are the quinquagintenary outcomes of the study?*
 57. *What are the sexagintenary outcomes of the study?*
 58. *What are the septuagintenary outcomes of the study?*
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 62. *What are the unsexagintenary outcomes of the study?*
 63. *What are the bisexagintenary outcomes of the study?*
 64. *What are the trisexagintenary outcomes of the study?*
 65. *What are the sexagintenary outcomes of the study?*
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 67. *What are the octogintenary outcomes of the study?*
 68. *What are the nonogintenary outcomes of the study?*
 69. *What are the trigintagintenary outcomes of the study?*
 70. *What are the unseptuagintenary outcomes of the study?*
 71. *What are the biseptuagintenary outcomes of the study?*
 72. *What are the triseptuagintenary outcomes of the study?*
 73. *What are the septuagintenary outcomes of the study?*
 74. *What are the octogintenary outcomes of the study?*
 75. *What are the nonogintenary outcomes of the study?*
 76. *What are the trigintagintenary outcomes of the study?*
 77. *What are the unoctogintenary outcomes of the study?*
 78. *What are the bioctogintenary outcomes of the study?*
 79. *What are the trioctogintenary outcomes of the study?*
 80. *What are the octogintenary outcomes of the study?*
 81. *What are the nonogintenary outcomes of the study?*
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 84. *What are the binonogintenary outcomes of the study?*
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 86. *What are the nonogintenary outcomes of the study?*
 87. *What are the trigintagintenary outcomes of the study?*
 88. *What are the unquadragintenary outcomes of the study?*
 89. *What are the biquadragintenary outcomes of the study?*
 90. *What are the triquadragintenary outcomes of the study?*
 91. *What are the quadragintenary outcomes of the study?*
 92. *What are the quinquagintenary outcomes of the study?*
 93. *What are the sexagintenary outcomes of the study?*
 94. *What are the septuagintenary outcomes of the study?*
 95. *What are the octogintenary outcomes of the study?*
 96. *What are the nonogintenary outcomes of the study?*
 97. *What are the trigintagintenary outcomes of the study?*
 98. *What are the unsexagintenary outcomes of the study?*
 99. *What are the bisexagintenary outcomes of the study?*
 100. *What are the trisexagintenary outcomes of the study?*

Db 545 gaagtcactggaggccaactgcactctgtag 575

RESULT 4

ID N60341 standard; DNA; 633 BP.

XX N60341;

13-JUN-1991 (first entry)

DE Sequence encoding salmon growth hormone variant of plasmid pSGH14.

XX SGH; E.coli; ds.

XX Oncorhynchus keta.

XX Key Location/Qualifiers
FT 1..633
FT /*tag= a

PN EP166444-A.

XX 02-JAN-1986.

XX 27-JUN-1985; 85EP-0107987.

XX 13-MAR-1985; 85JP-0050096.

XX 29-JUN-1984; 84JP-0134536.

XX 12-OCT-1984; 84JP-0213360.

XX 12-OCT-1984; 84JP-0213361.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX (SEKI/) SEKINE S.

XX Sekine S, Mizukami T, Sato M, Itoh S, Saito A;

XX WPI; 1986-008665/02.

XX P-PSDB; P60323.

XX Fish growth hormone poly-peptide - produced by culturing

XX microorganisms carrying recombinant DNA plasmid.

XX Claim 1; Table 2; 32pp; English.

XX The two variants of salmon growth hormone (pSGH1 and pSGH14) may be expressed from an E.coli host, and used for stimulating growth in cultivated fish.

XX Sequence 633 BP; 164 A; 173 C; 161 G; 135 T; 0 other;

Query Match 34.0%; Score 278.6; DB 7; Length 633;

Best Local Similarity 71.8%; Pred. No. 4.7e-70;

Matches 410; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

QY 255 AGACACACGAGCGCTTCAATATGACATCTGTTACACACCTGCACACAGCTGGC 314

Db 69 agaaaccaacgctctcaacatcgctcagtcggtgcaacatctccaccattggc 128

QY 315 TCAAAATGATTAAGACCTTTGAGGACAGCCTGTTGCTGAGGACGACAGCTGAG 374

Db 129 tcagaaatgttcaatgactttgacggtaccctgtgcctgtagaacgacgactgaa 188

QY 375 TAAATCTTCCTCTGCTCTTCTGCAATTCTGACTACATTGAGCGCCTGCTGGAAGA 434

Db 189 caagatatctctgctggactcttctaactgactccatcgtagcccgtagacaagca 248

QY 435 TGAACACAGAGAGCTCTATGCTGAGGCTTCTTCCATCTCTTTTCACTCTATGAGTC 494

Db 249 cgagactcagaagagtgctcagtgctgaagtgctccacatttcttcctgctgattgaatc 308

QY 495 CTGGGAGTTCCCAAGCCAGCTCCTGAGCGGAACCGTCTCAACAGACCTGACCGTAGGAA 554

Db 309 ctgggagtagccctagccagaccctg-----atcatctccaaagcctaattggtcagaaa 362

QY 555 CCCCAACACAGCTCAGTGAAGCTGGCCGACTTGAATGGGCATCAGTGTGCTCATCCA 614

Db 363 cgccaaaccagatctctgagagctcagcgaccccaagtggtggaatcaacctgctcatcac 422

QY 615 GGCATGCTCGATGGTCAACAAACATGATGATAACGACTCCTTGGCGGTG---CCTTTT 671

Db 423 ggggagccaggtggtgactgagcctggatgacaatgaactctcagcagctgccccctta 482

QY 672 TGAGGACTTCTTACTTGACCATGGGGGAGAAC---AACTCAGAGAGAGCTTTCGTCTGCT 728

Db 483 cgggaactactaccagaacctgggggagcgagaaacgtcagggaggaactacgagtgtt 542

QY 729 GGCTTGTCTCAAGAAGACATGCACAAAGTCGAGACCTACTTGAAGGTTGCAAAATTGCAG 788

Db 543 ggcattgttcaagaaggacatgcacaaggtcgagacctactgacctgaccgtcgcaagtgcag 602

QY 789 GAGATCCCTGGATTCCAACTGCACCTGTAG 819

Db 603 gaagtcactggaggccaactgcactctgtag 633

RESULT 5

Q38832

ID Q38832 standard; cDNA to mRNA; 1176 BP.

XX Q38832;

XX 28-JUL-1993 (first entry)

XX Pre-growth hormone from O. masou (Brevoort).

XX Recombinant; growth hormone; GH; transformant; ss.

XX Oncorhynchus masou (Brevoort).

XX Key Location/Qualifiers

FT 43..675

FT /*tag= a

FT /label= GH

FT mat_peptide 103..672

FT /*tag= b

FT polyA_signal 1136..1141

FT /*tag= c

PN JP05070496-A.

XX 23-MAR-1993.

XX 12-SEP-1991; 91JP-0260489.

XX 12-SEP-1991; 91JP-0260489.

XX (NIJI-) NIPPON JIIN KK.

XX WPI; 1993-131303/16.

XX P-PSDB; R34193.

XX Recombinant Oncorhynchus masou growth hormone - having specified

XX aminoacid sequence

XX Disclosure; Page 5-6; 6pp; Japanese.

XX The recombinant O. masou GH sequence can be used to prepare GH from

XX various transformants, in large amounts.

XX Sequence 1176 BP; 328 A; 261 C; 257 G; 330 T; 0 other;

XX Query Match 34.0%; Score 278.6; DB 14; Length 1176;

XX Best Local Similarity 71.8%; Pred. No. 5.9e-70;

Qy 729 GGCTTGCTTCAAGAGGACATGACAAAGTCGAGACCTACTTGGAGGTGCAAAATTGCAG 788
|||||
Db 607 ggccttgcttcaagaaggacatgcacaaagtcgagacctactctgacgcctgcgccaagtgcag 666
|||||
Qy 789 GAGATCCCTGGATTCCAACTGCACCTCTGTAG 819
|||
Db 667 gaagtcactggaggccaactgcactctgtag 697
|||||
RESULT 7
Q06417
ID Q06417 standard; DNA; 633 BP.
XX
AC Q06417;
XX
DT 05-FEB-1991 (first entry)
XX
DE Sequence encoding rainbow trout Growth hormone GH2.
XX
KW Fish growth hormone; salmon; FGH; SGH; ds.
XX
OS Salmo gairdneri.
XX
PN JP02243700-A.
XX
PD 27-SEP-1990.
XX
PF 17-MAR-1989; 89JP-0063594.
XX
PR 17-MAR-1989; 89JP-0063594.
XX
PA (NIUS) NIPPON SUISAN KAISHA.
XX
DR WPI; 1990-338513/45.
DR P-PSDB; R07642.
XX
FT Growth hormone gene of fish - contains polypeptide with specific
PT aminoacid sequence
XX
PS Disclosure; Fig 1; 8pp; Japanese.
XX
CC Fish growth hormone may be used to accelerate growth in cultured
CC fish.
XX
SQ Sequence 633 BP; 165 A; 176 C; 157 G; 135 T; 0 other;

Query Match 33.9%; Score 277.6; DB 11; Length 633;
Best Local Similarity 71.8%; Pred. No. 9e-70;
Matches 409; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

Qy 256 GACACACGCGGCTCTTCAATAATGAGTCATTCGTGTACACACCTGCACCGCTGGCT 315
|||
Db 70 gaaacacacgctcttcaacacgcggtcgaatccgctgcaacacacctccacctattgct 129
|||
Qy 316 GCAAAATGATTAACGACTTTGAGACACGCTTCCCTGAGACGCGAGACGCTGACT 375
|||||
Db 130 cagaaatgttcaacgactttgaagcaccctgttgcctgatgaacgcagacgctgaac 189
|||
Qy 376 AAAATCTTCCCTCTCTTCTTCTGCAATTCGTACTACATTCGAGCGGCTGCTGAAAAGAT 435
|||
Db 190 aagatatctctgctggaactctgtgaactctgactcctcatctgagcccaatcgacaagcag 249
|||
Qy 436 GAAACACAGAGAGCTCATGCTGAAGCTTCTTCGCATCTCTTTACCTCATTTGATGCC 495
|||
Db 250 gagactcagaagagtcagtcctgaagctgctccacatttcttccgctgctgactgaatcc 309
|||
Qy 496 TGGGAGTTCACAGAGCTCCCTGAGCGGAACCGTCTCAACAGCGCTGACCGTAGGGAAC 555
|||||
Db 310 tgggagtagcttagcagaccctg-----accatctccacagcctaagtgtcagaac 363
|||
Qy 556 CCCAACCGAGCTCACATGAGAGCTGGCCGCGACTTGAAATGGCATCAGTCTGCTCATCCAG 615
|||||

Db 364 tccaaccagatctctgagaagctcagcaccctcaaaagtggcatcaacacctgctcatcaag 423
Qy 616 GCATGCTCGATGGTCAACCAACATGGATGATGAAGACTCTCTTGGCGCTG---CCTTTT 672
|||
Db 424 gggagccagatggcgctactaagctggaatgacaatgactctcagcatctgccccctac 483
|||
Qy 673 GAGGACTTCTACTTGTACCATGGG---GAGAACAACCTCAGAGAGAGCTTTGCTCTGCTG 729
|||
Db 484 gggaaactactaccagaacctggggcgagcgcaacgctcaggagggaactacgagctgttg 543
|||
Qy 730 GCTTGTCTCAAGAAGGACATGCACAAAGTCGAGACCTACTTGGAGGTGCAAAATTGCAG 789
|||
Db 544 gcatgcttcaagaagtacatgataaggttgagacctacacctgacccgtcgccaagtgcag 603
|||
Qy 790 AGATCCCTGGATTCCAACTGCACCTCTGTAG 819
|||
Db 604 aagtatctggaggccaactgcactctgtag 633
|||
RESULT 8
N60340
ID N60340 standard; DNA; 633 BP.
XX
AC N60340;
XX
DT 13-JUN-1991 (first entry)
XX
DE Sequence encoding salmon growth hormone variant of plasmid pSGH1.
XX
KW SGH; E.coli; ds.
XX
OS Oncorhynchus keta.
XX
FH Key Location/Qualifiers
FT CDS 1..633
FT /*tag= a
XX
PN EP166444-A.
XX
PD 02-JAN-1986.
XX
PF 27-JUN-1985; 85EP-0107987.
XX
PR 13-MAR-1985; 85JP-0050096.
PR 29-JUN-1984; 84JP-0134536.
PR 12-OCT-1984; 84JP-0213360.
PR 12-OCT-1984; 84JP-0213361.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (SEKI/) SEKINE S.
XX
PI Sekine S, Mizukami T, Sato M, Itoh S, Saito A;
XX
XX WPI; 1986-008665/02.
DR P-PSDB; P60322.
XX
XX Fish growth hormone poly-peptide - produced by culturing
PT microorganisms carrying recombinant DNA plasmid.
XX
PS Claim 1; Table 2; 32pp; English.
XX
XX The two variants of salmon growth hormone (pSGH1 and pSGH14) may be
CC expressed from an E.coli host, and used for stimulating growth in
CC cultivated fish.
XX
SQ Sequence 633 BP; 164 A; 172 C; 162 G; 135 T; 0 other;

Query Match 33.8%; Score 277; DB 7; Length 633;
Best Local Similarity 71.6%; Pred. No. 1.3e-69;
Matches 409; Conservative 0; Mismatches 150; Indels 12; Gaps 3;

Qy 255 AGACACACGCGGCTCTTCAATAATGAGTCATTCGTGTACACACCTGCACCGCTGGC 314

Db 69 agaaacaaacgctcctcaacatgcggtcagtcggtgcaacatctccacattatggg 128
Qy 315 TCACAAATGATTACGACTTTGAGGACAGCTGTGGCTCGAGGACGACGAGCTGAG 374
Db 129 tcagaaatgttcaatgactttgacggtaccctgttgctgatgaaacgagacagctgaa 188
Qy 375 TAAATCTTCCCTCTGCTCTTCTGCAATTTCTGACTACATTTGAGGCGCTGCTGGAAGA 434
Db 189 caagatattctctggaacttctgtaactctgactccatctgagcccgagcagcaagca 248
Qy 435 TGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTACCTCATTTGAGTC 494
Db 249 cgagactcagaagagttcagtcctgaagctgctccacatttcttccgtctgattgaatc 308
Qy 495 CTGGGAGTTCCCAAGCAGCTGCTGAGCGGAACCGTCTCAACACAGCTGAGCGTAGGGAA 554
Db 309 ctggagagtaccctagccagaccctg-----atcatctccacagcctaatggctcagaa 352
Qy 555 CCCCACACAGCTACTGAGAGCTGGCCGACTTGAATAATGGGCATCAGTGTGCTCATCCA 614
Db 363 cgcaaccagactctgagaagctcagcgacctcaagtggtgcatcaacctgctcatcac 422
Qy 615 GGCATGCTCGATGTGTCACCAACATGATGATACGACTCTTGGCCGCTG---CCTTT 671
Db 423 ggggagccaggtggtgactgagctggtgataatgactctcagcagctgccccctca 482
Qy 672 TGAGGACTTCTACTTGACCATGGGGAGAAC---AACCTCAGAGAGAGCTTTCGTCTGCT 728
Db 483 cgggaactactaccgaacctgggggagcagcaggaacgtcagaggaactacgagttgtt 542
Qy 729 GCGTTGCTTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTCGAG 788
Db 543 ggcattctcaagaaggacatgcacaaggtcagacctcagcctgacccgtcgcaagtgcag 602
Qy 789 GAGATCCCTGGATTCCAACTGCACCCCTGTAG 819
Db 603 gaagtcactggaggccaaactgcactctgtag 633

RESULT 9

N70829
ID N70829 standard; DNA; 564 BP.
AC N70829;
XX
AC
XX
DT 13-JAN-1991 (first entry)
DE DNA encoding fish growth hormone.
XX Fish growth hormone; ss DNA; E.coli; plasmid pGEL1.
KW
XX
FH Key Location/Qualifiers
FT 1..564
CDS /*tag= a

JP6225500-A.

07-NOV-1987.

25-NOV-1986; 86JP-0J97842.

25-APR-1986; 86JP-0097842.

(KYOW) KYOWA HAKKO KOGYO KK.

WPI; 1987-352166/50.

P-PSDB; P70503.

Fish growth hormone polypeptide deriv. - prepd. by culturing microorganism transformed with recombinant DNA fragment.

Disclosure; Fig. 1 page 861; 11pp; Japanese.

XX Using the DNA, large amts. of fish growth hormone can be produced.
CC The DNA is inserted into a plasmid which can be expressed in E.coli,
CC eg pGEL1. The DNA is suitably the one shown, with bases 58-69
CC deleted. E.coli contg. pGEL1 is deposited as FERM BP-629.
CC It is cultivated at pH 5.5 - 8.5 at 18 - 40 deg C under aeration
CC and stirring.
XX
SQ Sequence 564 BP; 151 A; 160 C; 139 G; 114 T; 0 other;

Query Match 33.7%; Score 275.6; DB 8; Length 564;
Best Local Similarity 71.7%; Pred. No. 3.2e-69;
Matches 407; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

Qy 255 AGACAACCCAGCGCTCTTCAATATGAGTCAGTCATTCTGCTGATCAACACCTGCAACAGCTGGC 314
Db 3 agaaaacaaacgctctcaacatcgcggtcagtcggtgcaacatctccacattatggc 62
Qy 315 TGCAAAATGATTAAACGACTTTGAGGACAGCTGTTGCCCTGAGGAACGACAGCTGAG 374
Db 63 tcagaaaaatgttcaatgactttgacggtaccctgttgcctgatgaaacgagacagctgaa 122
Qy 375 TAAATCTTCCCTCTGCTCTTCTGCAATTTCTGACTACATTTGAGGCGCTGCTGGAAGA 434
Db 123 caagatattctctggaacttctgtaactctgactcctcagcagctgagcccgagcagcaagca 182
Qy 435 TGAACACAGAGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTACCTCATTTGAGTC 494
Db 183 cgagactcagaagagttcagtcctgagctgctccacatttcttccgtctgattgaatc 242
Qy 495 CTGGGAGTTCCCAAGCAGCTGCTGAGCGGAACCGTCTCAACACAGCTGACCGTAGGGAA 554
Db 243 ctgggaggtaccctagccagaccctg-----atcatctccacagcctcaatggctcagaa 296
Qy 555 CCCCACACAGCTACTGAGAGCTGGCCGACTTGAATAATGGGCATCAGTGTGCTCATCCA 614
Db 297 cgcaaccagactctgagaagctcagcgacctcaagtggtgcatcaacctgctcatcac 356
Qy 615 GGCATGCTCGATGTGTCACCAACATGATGATACGACTCTTGGCCGCTG---CCTTT 671
Db 357 ggggagccaggtggtgactgagctggtgataatgactctcagcagctgccccctca 416
Qy 672 TGAGGACTTCTACTTGACCATGGGGAGAAC---AACCTCAGAGAGAGCTTTCGTCTGCT 728
Db 417 cgggaactactaccgaacctgggggagcagcaggaacgtcagagggaactacgagttgtt 476
Qy 729 GCGTTGCTTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTCGAG 788
Db 477 ggcattctcaagaaggacatgcacaaggtcagacctcagcctgacccgtcgcaagtgcag 536
Qy 789 GAGATCCCTGGATTCCAACTGCACCCCTGTAG 816
Db 537 gaagtcactggaggccaaactgcactctg 564

RESULT 10

Q29359
ID Q29359 standard; cDNA; 1119 BP.
XX
AC
XX
AC
XX
DT 08-MAR-1993 (first entry)
DE Salmon growth hormone gene.
XX GH; transgenic; fish; antifreeze protein promoter; ss.
XX Oncorhynchus keta.
XX
FH Key Location/Qualifiers
FT 6..638
CDS /*tag= a

CC peptide-encoding sequence. A beta galactosidase- or gamma
 CC interferon-peptide can be used in place of the wsgH peptide. The
 CC resultant fusion protein is recovered from transformant host cells
 CC and the motilin component is easily isolated. This recombinant
 CC motilin is physiologically active and is used to activate intestinal
 CC movement (peristalsis). See also Q10875-77.

XX Sequence 555 BP; 150 A; 151 C; 135 G; 119 T; 0 other;

Query Match 26.5%; Score 217; DB 12; Length 555;
 Best Local Similarity 70.8%; Pred. No. 1.8e-52;
 Matches 305; Conservative 0; Mismatches 120; Indels 6; Gaps 1;

QY 255 AGACACACAGCGCTCTTCAATATGACGATCTTGTACACACCTGCACGAGTGGC 314

Db 6 aaaaaaacacggctctcaacatcggtcagtcggtgcaacatctcaactattggc 65

QY 315 TGCATAAATGATTACGACTTTGAGGACAGCGCTGTTGCCGTGAGGAACGCAGACGCTGAG 374

Db 66 tcagaaaatttcaatgactttgacggtaccctgttgctgtgataagcagacagctgaa 125

QY 375 TAAATCTTCCCTCTCTTTCGCAATTTGACTACTGACTGAGCGGCTGCTGGAAGA 434

Db 126 caagatattcctgctggaactctgttaactctgactccatcgtgagccagtcgacaagca 185

QY 435 TGAACACAGAGAGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTACCTCATTTGAGTC 494

Db 186 cgagactcagaagagttcagtcctgagctgagctccacattcttcctgctgattgaatc 245

QY 495 CTGGGAGTTCCCAAGCAGTCCCTGAGCGGAACCGCTCTCAACAGCGCTGACCGTAGGGAA 554

Db 246 ctgggagttaccctagcagaccctg-----atcatctcaacagcctaagtgcagaa 299

QY 555 CCCAACACAGCTCAGTGAAGCTGCCGACTTGAATAATGGGCGATCAGTGTGCTATCCA 614

Db 300 cggcaaacagatctctgagaagctcagcagcctcaagtgggcatcaacctgtctcatc 359

QY 615 GCATGCTCTCGATGTCACCAACATGATGATGATAACGACTCTCCCGCTGCTTTTGA 674

Db 360 ggggagcaggatggcgtactgagcctggatgacaaatgactctcagcagctgcccccta 419

QY 675 GGACTTTACT 685

Db 420 cgggaactact 430

RESULT 14

ID N70544

XX N70544 standard; DNA; 630 BP.

XX AC N70544;

XX DT 01-JAN-1980 (first entry)

XX DE Eel growth hormone.

XX XX Growth hormone; somatotropin; fish; plasmid pEGH15; ss.

XX OS Anguilla japonica.

XX PH Key Location/Qualifiers

FT sig_peptide 1..57

FT mat_peptide 58..627

FT /*tag= a

FT /*tag= b

PN EP209068-A.

XX 21-JAN-1987.

XX PF 09-JUL-1986; 86EP-0109346.

XX

PR 31-MAR-1986; 86JP-0074061.

PR 10-JUL-1985; 85JP-0151847.

PR 22-JUL-1985; 85JP-0161429.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Yamaguchi K, Saito A, Sekine S, Sato M, Itoh S, Shirahata K;

PI Hiranot, Hawauchi H;

XX WPI; 1987-015810/03.

DR P-PSDB; P70341.

XX New growth hormone extracted from eels - or prepd. by culturing

PT microorganisms transformed with new DNA coding sequences, used to

PT promote fish growth

XX Disclosure; Table 2; 58pp; English.

XX This sequence is contained in recombinant plasmid pEGH15 which may

CC be used to express the eel hormone in a bacterial host, e.g. E. coli.

CC The eel hormone has application in the stimulation of fish growth.

CC See also N70540 and N70544.

XX Sequence 630 BP; 161 A; 167 C; 158 G; 144 T; 0 other;

SQ

Query Match 24.8%; Score 203.2; DB 8; Length 630;

Best Local Similarity 61.8%; Pred. No. 1.6e-48;

Matches 341; Conservative 0; Mismatches 208; Indels 3; Gaps 1;

QY 268 CTCTTCAATATGACGACCTTCGTGTACACACCTGCACACGCTGGCTGCAAAATGATT 327

Db 82 ctcttcacagcgtgttaaccagacagacacgtgcacacactggtgcgaaataatac 141

QY 328 AACGACTTTGAGGACAGCGCTGTTGCCCTGAGGAACGCAGACAGCTGAGTAAATCTTCCT 387

Db 142 aaggaaatttgaggaagcattccacccagcagccacagacagctcagcaagacctcccca 201

QY 388 CTCTCTTTCTGCAATCTGACTACATTGAGCGCGCTCTGGAAGAAGATGAACACAGAG 447

Db 202 ttggcgggtgttactccgactccatccctacccccacagcagaagatgaacagcaggag 261

QY 448 AGCTATGCTGTAAGCTTCTTTCGCATCTCTTTTCCATCTGAGTCTGCGGAGTTCCCA 507

Db 262 aaatcgatgggtactgtgtgcacatctcctcagcctgatccagtcagtggtatctct 321

QY 508 AGCCAGTCTCTGAGCGGAACCGTCTCAACAGCGCTGACCGTAGGGAGACCCCAACAGCTC 567

Db 322 ttgaagacctgagcgtgttttcttaacagcgtgatttgggacctctgagggatc 381

QY 568 ACTGAGAGCTGGCGGACTTGAATAATGGGCATCAGTGTGCTCATCCAGGCATGCTCGAT 627

Db 382 ttgtataagctggagacacctgaacaaggatcaatgaatgaaggttggaggtagac 441

QY 628 GGTCAACCAACATGGATGATAACGACTCTCTTGCCTGCTGCTTTTGGAGGACTTCTACTTG 687

Db 442 ggtggtatttaccattgaggatgtgagaaatctccggtacagagaacttcagcgtcacact- 500

QY 688 ACCATGGGGGAGAACACACCTCAGAGAGAGCTTTCTGCTGTGGCTGTGCTCAAGAAGAC 747

Db 501 --taggaacgatgccggcctgatgaagaactatgctgctgcttcttaagaagacac 558

QY 748 ATGCACAAAGTCGAGACCTACTTGGAGGTTGCAAAATTCGAGGAGATCCCTCGATTCCAAC 807

Db 559 atgcacaaagtggagacctctacacgtgaaagtgcagcgctttgttagaagcaac 618

QY 808 TGCACCTGTAG 819

Db 619 tgcacctgtag 630

RESULT 15

N81504

ID N81504 standard; DNA; 630 BP.
XX AC N81504;
XX DT 14-SEP-1990 (first entry)
XX DE cDNA encoding GH-1.
XX KW GH-1; immunoglobulin-G agglutination activity.
XX FH Key Location/Qualifiers
XX FT CDS 1..630
XX FT /*tag= a
XX PN JP63214195-A.
XX PD 06-SEP-1988.
XX PF 28-FEB-1987; 87JP-0046595.
XX PR 28-FEB-1987; 87JP-0046595.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX DR WPI; 1988-290584/41.
XX DR P-PSDB; P81165.
XX PT Novel proteins and DNA sequences coding for them -
XX PT having immunoglobulin-G agglutination activity
XX PS Disclosure; Page 610; 30pp; Japanese.
XX CC The patent claims a protein having sequence 1, 13 or 15, and IgG
XX CC agglutination activity, DNA having nucleotide sequence encoding proteins
XX CC of sequences 1, 13 and 15, recombinant DNA comprising integrated DNA
XX CC encoding proteins of sequences 1, 13 and 15, and microorganisms
XX CC containing the recombinant DNA.
XX SQ Sequence 630 BP; 161 A; 168 C; 159 G; 142 T; 0 other;

Search completed: May 16, 2001, 10:06:21
Job time: 2614 sec

Query Match 24.8%; Score 203.2; DB 9; Length 630;
Best Local Similarity 61.8%; Pred. No. 1.6e-48;
Matches 341; Conservative 0; Mismatches 208; Indels 3; Gaps 1;
QY 268 CTCCTCAATATGACGCTTCCTGTACACACCTGCACGAGCTGGCTGCAAAATGATT 327
DB 82 ctcttcaccagcgctgttaaccgagcacagcacctgcacacactggtcggaatatatc 141
QY 328 AACGACTTTGAGGACAGCTGTGCTGAGGACGAGCAGCTGAGTAAATCTCCCT 387
DB 142 aaggaatttgagcagacatcccccagggccacacagcagctcagagacctcccca 201
QY 388 CTGCTCTTCTGCAATCTGACTACATTGAGCGCCTGCTGAAAAGATGAACACAGAAG 447
DB 202 ttggccgggtgttactccgactccatccctaccacagggcaagaatgaacgcaggag 261
QY 448 AGCTCTATGCTGAAGCTTCTTCGATCTCTTTACCTCATTTGAGTCTGGGAGTTCCCA 507
DB 262 aaatcgatgggtactgtctgcactctcctcagccctgacccagtcagtggtatcct 321
QY 508 AGCCAGTCCCTGAGCGGAACCGTCTCAACAGCCTGACCGTAGGGAACCCCAACCGCTC 567
DB 322 ctgaagacctgagcgatgctttctctaacagcctgatgtttgggacctctgatgggac 381
QY 568 ACTGAGAAGCTGGCCGACTGAAATGGGCATCAGTGTGCTCATCCAGGATGCTCGAT 627
DB 382 ttgtataagctgagggacctgaacaagggtcatcaatgaattaggttaggtgac 441
QY 628 GGTCAACCAACATGGATGATACGACTCCTTCCGCTGCTTTTGGAGGACTTCTACTTG 687
DB 442 ggtggtattatgaggtgagaaatctcccggtacgagaacttcgacgtacacct- 500

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OM nucleic - nucleic search, using sw model

Run on: May 16, 2001, 09:01:02 ; Search time 67.34 seconds
(without alignments)
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Title: US-09-402-488A-3
Perfect score: 819
Sequence: 1 ATCGGGGTTCTCATCATCA.....ATTCCAACTGCACCGCTAG 819

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0.

Searched: 302621 seqs, 87301344 residues
Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | | | | | |
|------------|---------|-------|--------|----|-------------------|--------------------|--|--|--|
| Result No. | Query % | | | DB | ID | Description | | | |
| | Score | Match | Length | | | | | | |
| 1 | 278.6 | 34.0 | 1201 | 1 | US-08-286-872-1 | Sequence 1, Appl | | | |
| 2 | 157.2 | 19.2 | 576 | 1 | US-08-093-383-4 | Sequence 4, Appl | | | |
| 3 | 152.4 | 18.6 | 601 | 1 | US-07-764-655D-6 | Sequence 6, Appl | | | |
| 4 | 152.4 | 18.6 | 601 | 1 | US-07-801-164A-3 | Sequence 3, Appl | | | |
| 5 | 152.4 | 18.6 | 603 | 1 | US-07-764-655D-7 | Sequence 7, Appl | | | |
| 6 | 150.8 | 18.4 | 576 | 1 | US-07-885-689A-28 | Sequence 28, Appl | | | |
| 7 | 150.8 | 18.4 | 579 | 1 | US-07-885-689A-36 | Sequence 36, Appl | | | |
| 8 | 150.8 | 18.4 | 579 | 1 | US-07-885-689A-37 | Sequence 37, Appl | | | |
| 9 | 147.2 | 18.0 | 755 | 1 | US-08-468-824-5 | Sequence 5, Appl | | | |
| 10 | 146.8 | 17.9 | 600 | 6 | 5514646-37 | Patent No. 5514646 | | | |
| 11 | 142.8 | 17.4 | 633 | 1 | US-08-388-267C-1 | Sequence 1, Appl | | | |
| 12 | 140.4 | 17.1 | 573 | 5 | PCT-US93-09232-1 | Sequence 1, Appl | | | |
| 13 | 140.4 | 17.1 | 579 | 1 | US-07-621-197C-1 | Sequence 1, Appl | | | |
| 14 | 140.4 | 17.1 | 579 | 1 | US-08-363-982-1 | Sequence 1, Appl | | | |
| 15 | 138.8 | 16.9 | 573 | 1 | US-07-963-331D-1 | Sequence 1, Appl | | | |
| 16 | 135.6 | 16.6 | 570 | 1 | US-07-963-331D-2 | Sequence 2, Appl | | | |
| 17 | 127.2 | 15.5 | 1240 | 1 | US-08-240-372-2 | Sequence 2, Appl | | | |
| 18 | 126.2 | 15.4 | 2732 | 6 | 5217891-14 | Patent No. 5217891 | | | |
| 19 | 126.2 | 15.4 | 2733 | 2 | US-08-846-021A-6 | Sequence 6, Appl | | | |
| 20 | 115 | 14.0 | 153 | 2 | US-08-679-865-41 | Sequence 41, Appl | | | |
| 21 | 115 | 14.0 | 153 | 2 | US-08-680-876-41 | Sequence 41, Appl | | | |
| 22 | 115 | 14.0 | 466 | 1 | US-08-457-245-20 | Sequence 20, Appl | | | |
| 23 | 115 | 14.0 | 1056 | 2 | US-08-701-191A-5 | Sequence 5, Appl | | | |
| 24 | 98.8 | 12.1 | 105 | 2 | US-08-687-865A-23 | Sequence 23, Appl | | | |
| 25 | 98.4 | 12.0 | 234 | 2 | US-08-687-865A-20 | Sequence 20, Appl | | | |
| 26 | 98 | 12.0 | 129 | 2 | US-08-679-865-38 | Sequence 38, Appl | | | |
| 27 | 98 | 12.0 | 129 | 2 | US-08-680-876-38 | Sequence 38, Appl | | | |

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|----|------|------|------|---|-------------------|--------------------|
| 28 | 96.8 | 11.8 | 2081 | 2 | US-09-096-982-7 | Sequence 7, Appl |
| 29 | 96.8 | 11.8 | 2081 | 2 | US-08-653-650A-7 | Sequence 7, Appl |
| 30 | 96.2 | 11.7 | 1599 | 3 | US-08-737-336-5 | Sequence 5, Appl |
| 31 | 96 | 11.7 | 96 | 3 | US-08-737-336-2 | Sequence 2, Appl |
| 32 | 93.4 | 11.4 | 762 | 4 | US-09-004-731-91 | Sequence 91, Appl |
| 33 | 93.4 | 11.4 | 762 | 4 | US-08-749-699-91 | Sequence 88, Appl |
| 34 | 93.4 | 11.4 | 811 | 4 | US-09-004-731-88 | Sequence 88, Appl |
| 35 | 93.4 | 11.4 | 811 | 4 | US-08-749-699-88 | Sequence 93, Appl |
| 36 | 91.8 | 11.2 | 783 | 4 | US-09-004-731-93 | Sequence 93, Appl |
| 37 | 91.8 | 11.2 | 783 | 4 | US-08-749-699-93 | Sequence 90, Appl |
| 38 | 91.8 | 11.2 | 823 | 4 | US-09-004-731-90 | Sequence 90, Appl |
| 39 | 91.8 | 11.2 | 823 | 4 | US-08-749-699-90 | Sequence 4, Appl |
| 40 | 90.4 | 11.0 | 3872 | 2 | US-08-331-081B-4 | Sequence 11, Appl |
| 41 | 87.4 | 10.7 | 1896 | 1 | US-08-605-541B-11 | Sequence 13, Appl |
| 42 | 83 | 10.1 | 838 | 1 | US-08-318-193-13 | Patent No. 5200327 |
| 43 | 83 | 10.1 | 846 | 6 | 5200327-5 | Sequence 29, Appl |
| 44 | 82.8 | 10.1 | 596 | 1 | US-07-826-928A-29 | Sequence 2, Appl |
| 45 | 82.2 | 10.0 | 579 | 1 | US-08-093-383-2 | |

ALIGNMENTS

RESULT 1
US-08-286-872-1
; Sequence 1, Application US/08286872
; Patent No. 5675061
; GENERAL INFORMATION:
; APPLICANT: Powers, Dennis A.
; TITLE OF INVENTION: Isolation and Characterization
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,872
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,272
; FILING DATE: 04-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 8600-0144.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1201 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Coho Salmon Growth Hormone Gene
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 65..697
; OTHER INFORMATION: /note= "Growth Hormone Precursor"
; FEATURE:

NAME/KEY: sig_peptide
LOCATION: 65..130
OTHER INFORMATION: /note= "growth hormone signal"
OTHER INFORMATION: peptide

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 131..697
OTHER INFORMATION: /note= "Growth Hormone"
US-08-286-872-1

Query Match 34.08; Score 278.6; DB 1; Length 1201;
Best Local Similarity 71.8%; Pred. No. 5.6e-76;
Matches 410; Conservative 0; Mismatches 149; Indels 12; Gaps 3;

QY 255 AGACAACAGCGGCTCTTCATATGATGAGTATTCGTTGATACACACCTGCACCTGGC 314
DB 133 AGAAAACCAAGCGCTCTCAACATGCGCGTCACTGCGGTGCAACATCTCCACCTATTGGC 192
QY 315 TGCAAAATGATTACGACTTTGAGGACAGCTGTTGCTGAGGAACGACAGCTGAG 374
DB 193 TCAGAAATGTTCAATGACTTTGAGGTACCTGTTGCTGATGAACGACAGCTGAA 252
QY 375 TAAATCTCTCTCTGCTTCTGCAATTCAGTATTCAGTATTCAGGCGCTGCTGGAAGA 434
DB 253 CAAGATATCTCTGCTGGACTTCTGTAATCTGACTCCATCTGAGCCGAGTCGACAAGCA 312
QY 435 TGAACACAGAGAGCTATGCTGAAGCTTCTTCGATCTCTTTTACCTCAATGAGTC 494
DB 313 CGAGACTCAGAAGAGTTGAGTCTGAGCTGCTCCATATTTCTTCCGCTGATTTGAATC 372
QY 495 CTGGAGTTCACAGGAGTCCCTGAGCGAGCTCTCAACAGCTGACGCTAGGAA 554
DB 373 CTGGAGTACCTGACGAGACCTG-----ATCATCTCCACAGCCTATGCTCGGAA 426
QY 555 CCCCAACAGCTCACTGAGAGCTGGCGGAGCTTGAATGGGCATCAGTGTGCTCATCCA 614
DB 427 CGCAACAGAGTCTGAGAGCTCAGGAGCTCAAGTGGGCATCAACCTGCTCATCAT 486
QY 615 GGCATGCTCATGGTCAACCAACATGATGATGAACAGCTTCCTGCGCTGCC---TTT 671
DB 487 GGGAGCGAGAGTGGCTGACTGAGCTGGATGACAAATGACTCTCAGAGCTGCCCGCTA 546
QY 672 TGAGGACTTCTACTTGACCTGGGGGAGAAC---AACCTCAGAGAGAGCTTTCGCTGCT 728
DB 547 CGGAAGTACTACAGAACCGGGGGGCGAGGAAAGCTCAGAGAGAACTACGAGTTGTT 606
QY 729 GGCTTGCTTCAAGAGGACATGCACAAAGTCGAGACCTACTTGAAGGTTGCAAAATGCG 788
DB 607 GGCTTGCTTCAAGAGGACATGCACAAGTTCGAGACCTACCTGACCGTCGCCAAGTCGAG 666
QY 789 GAGATCCCTGATTCCTCACTGCACCTCTAG 819
DB 667 GAAGTCACTGGAGGCCAACTGCACTCTGAG 697

RESULT 2
US-08-093-383-4
Sequence 4, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
APPLICANT: DeBoer, Herman A.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093.383
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/619827
FILING DATE: 28-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/632361
FILING DATE: 19-JUL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/303687
FILING DATE: 18-SEP-1981
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 46C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-093-383-4

Query Match 19.28; Score 157.2; DB 1; Length 576;
Best Local Similarity 56.5%; Pred. No. 6.9e-39;
Matches 313; Conservative 0; Mismatches 238; Indels 3; Gaps 1;
QY 266 GCCTCTTCAATATGACGATTCGTGTACACACCTGCACAGCTGGCTGCAAAATGA 325
DB 26 GTCATTCGCTAACGCTGTCTTCGTGCTCAGCATCTTCATCAGCTGGCTGACACCT 85
QY 326 TTAACGACTTTGAGGACGCTGTTGCCCTGAGGAAGCAGACAGCTGAGTAAATCTTCC 385
DB 86 TCAAGAGTTTGAGCGCACCTACATCCCGAGGAGACAGATACTCCATCCAGAACC 145
QY 386 CTCGTCTTCTGCAATTCGTACTACATTGAGGCGCTGCTGAAAGATGAACACAGA 445
DB 146 AGTTGCTCTTCTGCTTCTGTAACCATCCCGCCCCCGGCAAGGATGAGGCCAGC 205
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCTCTCTTTTCACTCATTTAGTCTGGAGTTCC 505
DB 206 AGAATCAGACTTGGAGCTGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 265
QY 506 CAAGCCAGTCCCTGAGCGGAGACCGTCTCAACAGCTGACCGCTAGGAGACCCACAGC 565
DB 266 CCCTGCAGTTCTCAGCAGAGTCTTCAACACAGCTGTTGTTGGCACCTCGGACG 325
QY 566 TCAGTCAAGAGCTGCGGAGCTTGAATGGGATGAGTGTGCTCATCCAGGAGTGTCTG 625
DB 326 TCATGAGAGAGTGAAGGAGCTGAGGAGGATCTCTGCGCTGATGCGGGAGCTGGAAG 385
QY 626 ATGGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 685
DB 386 ATGGACCCCGGGGCTGGGAGATCTCTCAAGCAGACCTATGACAAATTTGACACAA 445
QY 686 TGACCATGGGGAGGAACACCTCAGAGAGAGCTTTCGTCTGCTGGCTTGTCTCAAGAAG 745
DB 446 TCGGCA---GTACGACGCGCTGCTCAAGACTACGCTCTGCTCTCTCTCTCTCTCT 502

Matches 310; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATAATGACGATTCATGTCACACACCTGCACAGCTGGCTGCAAAATGA 325
DB 51 GCCTGTTTCCCAACGCTGTGCTCCGGGCTCAGACCTGCATGCTGGTGTGACACCT 110
QY 326 TTAACGACTTTGAGGACAGCCCTGTTCCCTGAGGACGCGACAGCTGAGTAAATCTTCC 385
DB 111 TCAAGAGTTTGAGCGCCTATACATCCCGGAGGACAGAGATCTCCATCCAGAACACC 170
QY 386 CTCCTCTTCTGCAATTCGTACTATGAGGCGCTGCTGAAAGATGAAACACAGA 445
DB 171 AGTTTGCCTTCTGCTTCTGAAACATCCCGGCCCCAGGCGCAAGATGAGGCCAGC 230
QY 446 AGAGCTCTATGCTGAGCTCTTCCGATCTCTTTCACTCTATGAGTCTGGAGTTCC 505
DB 231 AGAAATCAGACTTGGAGCTGTTCGATCTCACTGCTCTCATCCAGTCTGGTGGGC 290
QY 506 CAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGCCTGACCGTAGGGAACCCCAACAGC 565
DB 291 CCTCGAGTCTCTCAGCAGAGTCTTCAACACAGCTTGGTGTGACCTCGGACCGTG 350
QY 566 TCAGTGAAGCTGCGCGACTTGAATGGGATCAGTGTGCTATCCAGGAGTCTCTCG 625
DB 351 TCTATGAGAAGCTGAAGACCTGGAGGAGGATCTCTGCGCTGATGCGGGAGCTGGAAG 410
QY 626 ATGGTCAACCAACATGATGATAGGACTCTCTGCGCTGCTTTGAGGACTTCTACT 585
DB 411 ATGGCACCCCGCGCTGGGAGAGTCTCTCAAGCAGACCTATGACAAATTTGACACAAACA 470
QY 686 TGACCATGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGGCTTCTTCAAGAAGG 745
DB 471 TCGCA--GTGACAGCGCTGCTCAAGAACTACGCTCTGCTCTCTGCTTCCGGAAGG 527
QY 746 ACATGCACAAAGTCGAGACTACTTGAAGGTTGCAAAATTCAGGAGATCCCTGGATTCCA 805
DB 528 ACCTGCATAAGACGAGAGCTACCTGAGGTCATGAAGTGCCCGCTTCCGGGAGGCCA 587
QY 806 ACTGCACCTGTAG 819
DB 588 GCTGTGCTTCTAG 601

RESULT 5
US-07-764-655D-7/c
; Sequence 7, Application US/07764655D
; Patent No. 5378613
; GENERAL INFORMATION:
; APPLICANT: BELAGAJE, RAMA M.
; TITLE OF INVENTION: INCREASED EXPRESSION OF LOW MOLECULAR
; TITLE OF INVENTION: WEIGHT RECOMBINANT POLYPEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL CANTRELL 1116
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 5.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07764,655D
; FILING DATE: 19910924
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: JONES, JOSEPH A
; REGISTRATION NUMBER: 26,472
; REFERENCE/DOCKET NUMBER: X8031
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-764-655D-7

Query Match 18.6%; Score 152.4; DB 1; Length 603;
Best Local Similarity 56.0%; Pred. No. 2.1e-37;
Matches 310; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATAATGACGATTCATGTCACACACCTGCACAGCTGGCTGCAAAATGA 325
DB 555 GCCTGTTTCCCAACGCTGTGCTCCGGGCTCAGCAGCTGCACTGGCTGCTGACACCT 496
QY 326 TTAACGACTTTGAGGACAGCCTGTGCTGAGGAACGACAGAGCTCAGTAAATCTTCC 385
DB 495 TCAAGAGTTTGAGCGCCTATACATCCCGGAGGACAGAGATCTCCATCCAGAACACC 436
QY 386 CTCCTCTTCTGCAATTCGTACTATGAGGCGCTGCTGAAAGATGAAACACAGA 445
DB 435 AGTTTGCCTTCTGCTTCTGAAACCATCCCGGCCCCAGGCAAGATGAGGCCAGC 376
QY 446 AGAGCTCTATGCTGAGCTTCTTCCGATCTCTTTACCTCATGAGTGTCTGGAGTTCC 505
DB 375 AGAAATCAGACTTGGAGCTGCTTCCGATCTCACTGCTCTCATCCAGTCTGGCTTGGGC 316
QY 506 CAAGCCAGTCCCTGAGCGGAACCGTCTCAACAGCCTGACCGTAGGGAACCCCAACAGC 565
DB 315 CCTCGAGTCTCTCAGCAGAGTCTTCAACACAGCTTGGTGTGTCACCTCGGACCGTG 256
QY 566 TCAGTGAAGCTGGCGACTTGAATAATGGGCATGCTGCTCATCCAGGACTGTCTCG 625
DB 255 TCTATGAGAGCTGAAGGACTGGAGGAAGCATCTTGGCCCTGATCGGGAGCTGGAAG 196
QY 626 ATGGTCAACCAACATGAGTATGATGAGCTCTTTCGCGCTGCTTTGAGGAGCTTCTACT 685
DB 195 ATGGCACCCCGCGCTGGGAGATCTCTCAAGCAGAGACTATGACAAATTTGACACAAACA 136
QY 686 TGACCATGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGGCTTCTTCAAGAAGG 745
DB 135 TCGCA--GTGACAGCGCTGCTCAAGAACTACGCTCTGCTCTCTGCTTCCGGAAGG 79
QY 746 ACATGCACAAAGTCGAGACTACTTGAAGGTTGCAAAATTCAGGAGATCCCTGGATTCCA 805
DB 78 ACCTGCATAAGACGAGAGCTACCTGAGGTCATGAAGTGCCCGCTTCCGGGAGGCCA 19
QY 806 ACTGCACCTGTAG 819
DB 18 GCTGTGCTTCTAG 5

RESULT 6
US-07-885-689A-28
; Sequence 28, Application US/07885689A
; Patent No. 5365876
; GENERAL INFORMATION:
; APPLICANT: Cho, Joong M.
; APPLICANT: Lee, Tae H.
; APPLICANT: Chung, Hyun H.
; APPLICANT: Lee, Yong B.
; APPLICANT: Lee, Tae G.
; APPLICANT: Park, Young W.
; APPLICANT: Han, Kyu B.
; TITLE OF INVENTION: Method for Production of Bovine Growth
; TITLE OF INVENTION: Hormone Using a Synthetic Gene.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch

STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,689A
FILING DATE: 19-MAY-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 377-144P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE: Bovine
FEATURE:
NAME/KEY: CDS
LOCATION: 1..573
OTHER INFORMATION: /product= "Bovine growth hormone"
US-07-885-689A-28

Query Match 18.4%; Score 150.8; DB 1; Length 576;
Best Local Similarity 55.8%; Pred. No. 6.3e-37;
Matches 309; Conservative 0; Mismatches 242; Indels 3; Gaps 1;
QY 266 GGCTCTTCAATATGACGATTCGTTGTTGACACACCTGCACACCTGGCTGGTCAAAAATGA 325
DB 26 GTCATTCGCTAACGCTGTTCTCGAGCTCAGCATCTTCATCAGCTGGCTGCTGACACCT 85
QY 326 TTAACGACCTTCAGACACACCTGTTGCTCGAGAGGAGCAGCAGCTGAGTAAATCTTC 385
DB 86 TCAAAGAGTTTCAGCGCACCTACATCCCGAGGAGCAGAGATCTCCATCCAGAACACCC 145
QY 386 CTCCTGCTTCTGCAATTCGATCATGAGCGGCTGCTGAAAGATGAACACAGA 445
DB 146 AGTTGCTCTGCTCTGATGACCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 205
QY 446 AGAGCTCTATGCTGAGCTTCTTCGATCTCTTTTCAACCTCATTTGAGTCTCTGGAGTTCC 505
DB 206 AGAATCAGACTTGGAGCTGCTGCTGATCTCTGATCTGATCCAGCTGCTGCTCGGC 265
QY 506 CAAGCCAGCTCCTGAGCGGAACCTCTCAACAGCCTGACCGTAGGAGACCCCAACAGC 565
DB 266 CCCTGAGTCTCTCAGCAGAGAGCTTTCACCAACAGCTTGTGTTGCTGCTGAGCCGCTG 325
QY 566 TCACGTGAGAGCTGCCGACTTGAATATGGGATGATGCTGCTGATCCAGGATGCTCTCG 625
DB 326 TCTATGAGAGCTGAGGATCTAGAGGAGGATCTTGGCCCTGATGCGGGAGCTGGAG 385
QY 626 ATGGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 685
DB 386 ATGGCACCCTCCGCTGGGAGAGCTCTCAACAGCCTATGACAAATTTGACACAAACA 445
QY 686 TGACCATGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTG 745
DB 446 TGCGCA---GTGACGACGCGTGTCTCAAGAACTACGGTCTGCTCTCTCTCTCTCTCTCT 502

QY 746 ACATGCACAAATCGAGACCTACTTGAGGTTGCAAAATTGCAGGAGATCCCTGGATTCCA 805
DB 503 ACCTGCATAGACGAGACGTACCTGAGGGTCATGAGTGCCTTCGGGGAGGCCA 562
QY 806 ACTGCACCTCTAG 819
DB 563 GCTGCGCTTCTAG 576
RESULT 7
US-07-885-689A-36
Sequence 36, Application US/07885689A
Patent No. 5366876
GENERAL INFORMATION:
APPLICANT: Cho, Joong M.
APPLICANT: Lee, Tae H.
APPLICANT: Chung, Hyun H.
APPLICANT: Lee, Yong B.
APPLICANT: Lee, Tae G.
APPLICANT: Park, Young W.
APPLICANT: Han, Kyu B.
TITLE OF INVENTION: Method for Production of Bovine Growth
TITLE OF INVENTION: Hormone Using a Synthetic Gene.
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolash & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,689A
FILING DATE: 19-MAY-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 377-144P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY:
LOCATION: 1..60
OTHER INFORMATION: /label= 5'/end
OTHER INFORMATION: /note= "5' proximal sequence of BGH Insert in
OTHER INFORMATION: ptpshBGH1-13, shown in Fig...."
US-07-885-689A-36

Query Match 18.4%; Score 150.8; DB 1; Length 579;
Best Local Similarity 55.8%; Pred. No. 6.4e-37;
Matches 309; Conservative 0; Mismatches 242; Indels 3; Gaps 1;
QY 266 GGCTCTTCAATATGACGATTCGTTGTTGACACACCTGCACACCTGGCTGGTCAAAAATGA 325
DB 29 GTCATTCGCTAACGCTGTTCTTCGAGCTCAGCATCTTCATCAGCTGGCTGCTGACACCT 88

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER, FRANK & SCHNEIDER
STREET: 1111 Nineteenth St., N.W.,
CITY: Washington
STATE: DC
COUNTRY: US
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,824
FILING DATE: 14-FEB-1990

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/134,946
FILING DATE: 12-OCT-1993
APPLICATION NUMBER: US 07/984,244
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/171,179
FILING DATE: 18-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/480,051
FILING DATE: 14-FEB-1990

REGISTRATION NUMBER: 26,031
REFERENCE/DOCKET NUMBER: CARPR 0025C3
TELEPHONE: (202) 828-8000
TELEFAX: (202) 828-8038
TELEX: SPENCER 64267
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 63...635
PUBLICATION INFORMATION:
DOCUMENT NUMBER: GB 8701848
FILING DATE: 28-JAN-1987

US-08-468-824-5

Query Match 18.0%; Score 147.2; DB 1; Length 755;
Best Local Similarity 55.4%; Pred. No. 9.3e-36;
Matches 306; Conservative 0; Mismatches 243; Indels 3; Gaps 1;

Qy 268 CTCCTCAATATGACGATCTTCGTGTACAAACACGACGCTGAGTAAATCTCCCT 387
Db 90 CTGTTGCGTAAGCTGTTCTGGGCGCCACGACCTGACCAAACTGGCTGCCGACACTAC 149

Qy 328 AACGACTTTGAGGACAGCCTGTTCGTGAGGACGACGACGCTGAGTAAATCTCCCT 387
Db 150 AAGGAGTTGAGCGCGCTTACATCCCGGAGGACGACGAGGATCTCCATCCAGAACGCCAG 209

Qy 388 CTGCTTTCTCAATCTGACTACATATTGAGGCGCTGTGGGAAAGAGTGAACACAGAGAG 447
Db 210 GCTGCTTCTGCTCTCGGAGACCATCCCGGCGCCACGCGGCAAGGACGAGGCCAGCAG 269

Qy 448 AGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTCACCTCATTGAGTCTCGGAGTTCCTCA 507
Db 270 AGATCGGACGTGAGCTGCTGCGCTTCTCGCTGCTTCATCCAGTCTGCTGGGCCCC 329

Qy 508 AGCAGTCCCTGAGCGGAACCGTCTCAACAGCCTGACCCGTAGGGAACCCCAACAGCTC 567
Db 330 GTGCAAGTCTCAGCAGGGTCTTCAACCAACAGCCTGGTGTGTCACCTCAGACCGGCTC 389

Qy 568 ACTGAGAAGCTGCGCGACTTTGAAAATGGGATAGTGTGCTCATCCAGGATGCTCCAT 627
Db 390 TACGAGAAGCTGAGGACCTGGAGAGGGATCCAGGCCCTGATCGGAGCTGGAGAT 449

Qy 628 GGTCAACCAAACTGGATGATAACGACTCCTTGCGCGTGCCTTTTGAGGACTTCTACTTG 687
Db 450 GGCAGCCCCCGGACGACAGATCCTCAAGCAACCTACGACAAATTTGACACAACTTG 509

Qy 688 ACCATGGGGGAGAACACCTTCAGAGAGAGCTTTCTGCTGCTGGCTTCTCAAGAAGGAC 747
Db 510 CGCA--GTGATGACGGCTGCTTAAGAACTACGGGCTGCTCTCTCTCAAGAAGGAC 566

Qy 748 ATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTCAGGAGATCCCTCGATTCCAA 807
Db 567 CTGCAAAAGCTGAGACATACCTGCGGGTCAATGAAGTGTGCGCGCTTCTGAGAGCAGC 626

Qy 808 TGCACCTGTAG 819
Db 627 TGTGCTTCTAG 638

RESULT 10
5514646-37
; Patent No. 5514646
; APPLICANT: CHANCE, RONALD E.; DIMARCHI, RICHARD D.; FRANK,
; BRUCE H.; SHIELDS, JAMES E.
; TITLE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION
; 29 OF THE B CHAIN
; NUMBER OF SEQUENCES: 52
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,201
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,632
; FILING DATE: 17-APR-1991
; APPLICATION NUMBER: 388,201
; FILING DATE: 04-AUG-1989
; APPLICATION NUMBER: 308,352
; FILING DATE: 09-FEB-1989
; SEQ ID NO: 37
; LENGTH: 600
5514646-37

Query Match 17.9%; Score 146.8; DB 6; Length 600;
Best Local Similarity 56.5%; Pred. No. 1.1e-35;
Matches 313; Conservative 0; Mismatches 237; Indels 4; Gaps 2;

Qy 266 GGCTCTCAATATGACGATCTTCGTGTACAAACACCTGACCCAGCTGGCTGCAAAAATGA 325
Db 51 gcctgtttgcaacgctgtgctcgggctcagcaccctgcatcagctgctgctgacacct 110

Qy 326 TTAACGACTTTGAGGACAGCCTGTTCGTGAGGAAACGACGACGCTGAGTAAATCTTCC 385
Db 111 tcaagagtttgagcgcaacctacatcccgaggagacagagatactccatccagacacc 170

Qy 386 CTCGTGCTTCTCAATCTGACTACATATTGAGGCGCTGTGGAAAGAGATCAAAACAGA 445
Db 171 agttgctctctgctctctgaaacccatcccgccccacggcgaagatgagccagc 230

Qy 446 AGAGCTCTATGCTGAAGCTTCTTCGATCTCTTTACCTCATTTGCTGGGAGTTCC 505
Db 231 agaaatcagacttgagctgctgcatctcactgctcctcactcagctcgtgctggtgccc 290

Qy 506 CAAGCCAGTCCCTGAGCGGAACCGTCTCAAAACAGCCTTGACCGCTAGGGAACCCCAACAGC 565

Db 291 cctg-cagttctcagcagagcttccacacagagctgtgttggcaccctcgggacccgtg 349
Qy 566 TCACGTGAGAAGCTGCCGCACTTGAATGGGATCAGTGTGCTCATCCAGGATCTCTCG 625
Db 350 tctatgagaagctgaagcctcgggaagcctcctgctcctgctgagcgggagctggaag 409
Qy 626 ATGCTCAACCAACATGATGATACGACTCTTCCCGCTGCTTTTGAGGACTTCTACT 685
Db 410 atggcaccctccgctggcgagatccctcaagcagacctatgacaaatttgacacaaaca 469
Qy 686 TGACCATGGGGAGAGAACACCTCAGAGAGAGCTTTCGTCTGCTGGCTTCTTCAAGAAGG 745
Db 470 tgcgca---gtgacagcgcgtgctcagaagactcaggtctctctcctgcttcccggaag 526
Qy 746 ACATGCACAAAGTCGAGACCTACTTTCAGGGTTGCAAAATTCAGAGAGATCCCTGGATTC 805
Db 527 acctataagacggagcgtacctcaggtgaggtcatgaagtgcgcgcttcggggagccca 586
Qy 806 ACTGCACCTCTAG 819
Db 587 gctgtgcctctag 600

RESULT 11

US-08-388-267C-1
; Sequence 1, Application US/08388267C
; Patent No. 5866268

; GENERAL INFORMATION:
; APPLICANT: JONES, ELAINE V.
; APPLICANT: SATHE, GANESH M.
; APPLICANT: O'BRIEN, SHAWN
; APPLICANT: CLARK, MICHAEL T.
; APPLICANT: ALILA, HECTOR W.
; APPLICANT: MILLER, TIMOTHY J.
; TITLE OF INVENTION: FUSION PROTEINS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PFIZER INC.
; STREET: 235 EAST 42ND STREET
; CITY: NEW YORK
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10017-5755
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,267C
; FILING DATE: 27-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLLER, ALAN L.
; REGISTRATION NUMBER: 37,371
; REFERENCE/DOCKET NUMBER: PC9042A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-573-2118
; TELEFAX: 212-808-8893
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Sus scrofa
; TISSUE TYPE: Pituitary gland
; IMMEDIATE SOURCE:

; CLONE: PGH-1/PGH-2
US-08-388-267C-1

Query Match 17.4%; Score 142.8; DB 1; Length 633;
Best Local Similarity 54.9%; Pred. No. 1.9e-34;
Matches 304; Conservative 0; Mismatches 247; Indels 3; Gaps 1;
Qy 266 GGCTCTTCAATATGACGATTCGTGTATACACACCTGCACACAGCTGGTGCAAAATGA 325
Db 83 GCCTATTTCACACGCGTGTCTCCGGGCCACGACCTGCACCACTGGTGGCCACACT 142
Qy 326 TTAACACACTTTGAGGACAGCTTTCCTGAGGAAGCAGACAGCTGAGTAAATCTCC 385
Db 143 ACAAGAGAGTTTGAAGCGGCTTACATCCCGAGGGACAGAGGTACTCTCATCAAGACGCC 202
Qy 386 CTCTGTCTTCTGCAATTCGTACTACATTCAGGCGCTCTGGAAGATGGAAGATGAACACAGA 445
Db 203 AGCTCGCTTCTGCTTCTCGGAGACCATCCCGGCCCCACGAGGAGGCCCGCAGC 262
Qy 446 AGAGCTCTATGCTGAAGCTTTCGCACTCTTTTACCTCATTCATTCCTGGAGTTCC 505
Db 263 AGAGATCGGACGTGGAGCTGCTGGCTTCTGCTGCTCATCCAGTCTGCTGGCTCGGC 322
Qy 506 CAAGCCAGTCCCTGAGCGGACCTCTCAACACAGCTGACCGTAGGGAACCCCAACAGC 565
Db 323 CGGTGAGTTCCTCAGCAGGGTCTTCAACACAGCTGCTTGGGACCTTCAGACCGCG 382
Qy 566 TCACCTGAGAAGCTGGCGGACTTGAATATGGCATTCAGTGTGCTCATCCAGGATGTCTCG 625
Db 383 TCTACGAGAAGCTGAAGGACCTGGAGGAGGCATCCAGGCCCTCATCGGGAGTGGAG 442
Qy 626 ATGGTCAACCAACATGGATGATACGACTCTTTCGCGCTGCGCTTTTGGAGACTTCTACT 685
Db 443 ATGGCAGCCCCGGGAGGAGACATCTCAAGCAAACTACGACAAATTTGACACAACT 502
Qy 686 TGACCATGGGGAGAACACCTCAGAGAGCTTTCGTCTGCTGGCTTCTCAAGAAGG 745
Db 503 TGGGCA---GTGATGACGCGCTGCTTAAGAACTACGCGCTGCTCTCTCTTCAAGAAGG 559
Qy 746 ACATGCACAAAGTCGAGACCTACTTGAGGGTTGCAAAATTCAGAGAGATCCCTGGATTC 805
Db 560 ACCTGCACAGGCTGAGACATACCTGCGGGTCTGAGTGTGCGCGCTTCGTGGAGAGCA 619
Qy 806 ACTGCACCTCTAG 819
Db 620 GCTGTGCTTCTAG 633

RESULT 12

PCT-US93-09232-1
; Sequence 1, Application PC/TUS9309232
; GENERAL INFORMATION:
; APPLICANT: The Upjohn
; APPLICANT: Company
; TITLE OF INVENTION: Somatotropin Modifications
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Corporate Intellectual Property Law
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette (DS, HD 2.0 Mb)
; COMPUTER: IBM PC compatible WIN 386
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09232
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 2
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: James D. Darnley, Jr.
REGISTRATION NUMBER: 33673
REFERENCE/DOCKET NUMBER: 4766.P CNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616 385 5210
TELEFAX: 616 385 6897
TELEX: 224 401 UPJOHN
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: nucleotide
LENGTH: 573 base pairs
STRANDEDNESS: double stranded
TOPOLOGY: linear
PCT-US93-09232-1

Query Match 17.1%; Score 140.4; DB 5; Length 573;
Best Local Similarity 54.7%; Pred. No. 9.8e-34;
Matches 301; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATATGACGATCTGCTGTAACACACCTGCACACGCTGGCTGCAAAATGA 325
DB 26 GCCTATTTGCCAAGCGCTGCTCGGGCCAGCACCTGCACCAACTGGCTGCCGACACT 85
QY 326 TTAACGACTTTGAGGACACGCTGTTCCCTGAGGAACGACAGCTGAGTAAATCTTCC 385
DB 86 ACAAGAGTTTGGCGCGCTTACATCCCGAGGGAGACAGAGTACTCCATCCAGAACGCC 145
QY 386 CTCCTGCTTCTGCAATTCGACTACATGAGCGCTGCTGAAAGATGAAACACAGA 445
DB 146 AGGCTGCTTCTGCTTCTCGGAGACCATCCCGCCCCCAGGAGGAGGAGGCCAGC 205
QY 446 AGAGCTATGCTGAAGCTTCTTCGCACTCTTTTTCACCTCATTTGAGTCTCTGGAGTTC 505
DB 206 AGAGATCGGACGTTGGAGCTGCTGCGCTTCTCGCTGCTGCTCATCCAGTCTGCTCGGC 265
QY 506 CAAGCAGTCCCTGAGCGAAGCTGCTCAACAGCCTGACCGTAGGGAACCCCAACAGC 565
DB 266 CGCTGCACTTCTGACGAGGCTTTCACCAACAGCCTGCTGTTTGGCACCCTCAGACCGC 325
QY 566 TCACGTGAGAGCTGGCGACTTGAATGGCATGAGTGTCTATCCAGGSCATGCTCG 625
DB 326 TCTAGAGAGCTGAAGACCTGAGGAGGAGGATCCAGGCCCTTGTGCGGAGCTGGAGG 385
QY 626 ATGGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 685
DB 386 ATGGCAGCCCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 445
QY 686 TGACCATGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 745
DB 446 TCGGCA--GTGACGCGCTGCTTAAGAACTACGCGGCTGCTCTCTCTCTCTCTCTCTCT 502
QY 746 ACATGACAAAGTGCAGACCTACTTACGAGGTTGCAATTTGACGAGGATCCCTGATCCA 805
DB 503 ACCTGCAAGGCTGAGACATACCTCGGGTGTATGAAGTGTCTGCCGCTTCTGCGGAGGCA 562
QY 806 ACTGCACCT 815
DB 563 GCTGTGCTT 572

RESULT 13
US-07-621-197C-1
Sequence 1, Application US/07621197C
Patent No. 5310882
GENERAL INFORMATION:
APPLICANT: Chaleff Dr., Deborah T.
TITLE OF INVENTION: Somatotropins with Alterations in the
TITLE OF INVENTION: Alpha-Helix 3 Region, Alpha-Helix 2 Region Combinations

TITLE OF INVENTION: Thereof, and in Combination with Other Mutations
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street
CITY: Stamford
STATE: CT
COUNTRY: United States of America
ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/621.197C
FILING DATE: 19901130
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tsevdos Dr., Estelle J.
REGISTRATION NUMBER: 31,145
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2756
TELEFAX: 203-321-2971
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..579
US-07-621-197C-1

Query Match 17.1%; Score 140.4; DB 1; Length 579;
Best Local Similarity 54.7%; Pred. No. 9.9e-34;
Matches 301; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATATGACGATCTGCTGTAACACACCTGCACACGCTGGCTGCAAAATGA 325
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QY 386 CTCTGCTTTTTCGAATTCGACTACATTTGAGGCGCTGCTGGAAGAGTGAACACAGA 445
DB 152 AGGCTGCTTCTGCTTCTCGGAGACCATCCCGCCCCCAGGAGGAGGAGGAGGAGGAGG 211
QY 446 AGAGCTATGCTGAAGCTTCTTCGCACTCTTTTTCACCTCATTTGAGTCTCTGGAGTTC 505
DB 212 AGAGATCGGAGCTGGAGCTGCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
QY 506 CAAGCCAGTCCCTGAGCGGACCGCTCTCAACACGCTGACCTGAGGAACCCCAACAGC 565
DB 272 CGGTGCACTTCTCGAGGAGTCTTACCAACAGCGCTGTTGTTGCGACCTCAGACCGGG 331
QY 566 TCACTGAGAGCTGGCGACTTGAATAATGGGATGCTGCTCATCCAGGAGTCTCTCG 625
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QY 626 ATGTCAACCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 685
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Db 452 TCGCA---GTGATGACGGCTCTTAAGACTACGGGTGCTCTCTCTCTCAAGAGG 508
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QY 806 ACTGCACCT 815
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RESULT 14

US-08-363-982-1
; Sequence 1, Application US/08363982
; Patent No. 5348068
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; APPLICANT: Lebens, Michael R.
; APPLICANT: Chaleff, Deborah T.
; TITLE OF INVENTION: Somatotropins with Alterations in the
; TITLE OF INVENTION: Alpha-Helix 1 Region, and Combinations with Other
; TITLE OF INVENTION: Mutations
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,982
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,405
; FILING DATE: 28 JAN 1993
; APPLICATION NUMBER: US/07/621,656
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38360/JPW/LSW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 Coop ul
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..579
US-08-363-982-1

Query Match 17.1%; Score 140.4; DB 1; Length 579;
Best Local Similarity 54.7%; Pred. No. 9.9e-34;
Matches 301; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

QY 266 GCTCTTCAATATGAGTCATTGTGTACACACCTGCACAGCTGGGTGCAAAATGA 325
Db 32 GCCTATTGCCAAGCCGTGCTCCGGGCCAGCACCTGCACCACTGGTGGCGACACT 91

QY 326 TTAACGACTTTGAGCAGACCTGTTGCTGAGGAACGAGACAGCTGAGTAAATCTTCC 385
Db 92 ACAGGAGTTTGAGCGCCCTACATCCGGAGGAGGAGGTACTCTCATCCAGAACGCC 151
QY 386 CTCTGTCTTTCTCAATTTCTGACTACATTTGAGGCGCTGCTGGAAAAGATGAAACACAGA 445
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QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTACCTCATTTAGTCTCTGGAGTTCC 505
Db 212 AGAGATCGGAGCTGGAGCTGCTGCTGCTCTGCTGCTGCTCATCCAGTCTGCTGGGC 271
QY 506 CAAGCCAGTCCCTGAGCGGAACCGTCTCAACACGCTGACCGTAGGGAAACCCCAACACAGC 565
Db 272 CCGTGCAGTTCTCAGCAGGGTCTTACCAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
QY 566 TCACTGAGAAAGCTGGCGCACTTGAAATGGGCATCAGTGTCTCATCCAGGACATGCTCTCG 625
Db 332 TCTACGAGAAGCTGAAGCACTGGAGGAGGCACTCCAGGCCCTGATCGGGAGCTGGAGG 391
QY 626 ATGCTCAACCAACATGATGATTAACGACTCTTTCGCGCTGCTTTTGGAGACITCTACT 685
Db 392 ATGCGACGCCCGGCGAGGACATCTCTCAAGCAAACTACGACAAATTTGACACAAAT 451
QY 686 TGACCATGGGGAGAACAACTCAGAGAGAGCTTTGCTGCTGCTGCTGCTTCAAGAAGG 745
Db 452 TGGCA---GTGATGACGCGCTGCTTAAGAACTACGGGCTGCTCTCTCTCTCAAGAAGG 508
QY 746 ACATGCACAAAGTCGAGACCTTACTTGGGGTTGCAAAATTCGAGGAGATCCCTGGATTCCA 805
Db 509 ACCTGCACAAAGCTGAGACATACCTCGGGTCAATGAAGTGTCCGCGCTTCTGTTGGAGAGCA 568
QY 806 ACTGCACCT 815
Db 569 GCTGTGCTT 578

RESULT 15

US-07-963-331D-1
; Sequence 1, Application US/07963331D
; Patent No. 5334511
; GENERAL INFORMATION:
; APPLICANT: Harada, Yasuhiro
; APPLICANT: Nakano, Eiichi
; APPLICANT: Tatsumi, Hiroki
; APPLICANT: Umez, Motoaki
; TITLE OF INVENTION: Isolated Mink Growth
; TITLE OF INVENTION: Hormone Genes, No. 5334511el Recombinant DNA And
; TITLE OF INVENTION: Methods For Producing Mink Growth Hormone.
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/963,331D
; FILING DATE: 19921016
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Derigostis, Michael E.
; REGISTRATION NUMBER: 31,243
; REFERENCE/DOCKET NUMBER: HIRA-00600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150

Search completed: May 16, 2001, 10:03:58
Job time: 3776 sec

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193: em_gss_rod1:*
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233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 147.2 | 18.0 | 285 | 18 | AI308622 |
| 2 | 147.2 | 18.0 | 570 | 139 | BE755837 |
| 3 | 138 | 16.8 | 280 | 18 | AI308623 |
| 4 | 128.4 | 15.7 | 517 | 139 | BE755987 |
| 5 | 124 | 15.1 | 547 | 118 | AW659506 |
| 6 | 124 | 15.1 | 547 | 143 | BF077176 |
| 7 | 124 | 15.1 | 553 | 139 | BE756195 |
| 8 | 124 | 15.1 | 576 | 118 | AW631765 |
| 9 | 123.8 | 15.1 | 497 | 150 | BF605397 |
| 10 | 120.6 | 14.7 | 477 | 151 | BF65271 |
| 11 | 117.6 | 14.4 | 476 | 140 | BE861283 |
| 12 | 117.2 | 14.3 | 261 | 114 | AW330514 |
| 13 | 115 | 14.0 | 697 | 107 | AU170721 |
| 14 | 115 | 14.0 | 773 | 107 | AU167389 |
| 15 | 114.6 | 14.0 | 495 | 118 | AW657301 |
| 16 | 114.6 | 14.0 | 549 | 118 | AW655562 |
| 17 | 114.4 | 14.0 | 502 | 139 | BE756401 |
| 18 | 112.8 | 13.8 | 535 | 161 | BE030382 |

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| 19 | 112.8 | 13.8 | 548 | 145 | BF193497 | BF193497 | 245105 | MA |
| 20 | 112.8 | 13.8 | 561 | 120 | AW785352 | AW785352 | 116318 | MA |
| 21 | 112.8 | 13.8 | 641 | 168 | BF711364 | BF711364 | MI-P-A1-a | |
| C 22 | 112.6 | 13.7 | 532 | 116 | AW492282 | AW492282 | UI-N-BH3- | |
| C 23 | 111.2 | 13.6 | 575 | 168 | BF7112372 | BF7112372 | MI-P-A3-a | |
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| C 25 | 108.2 | 13.2 | 485 | 151 | BF651373 | BF651373 | 274072 | MA |
| 26 | 108 | 13.2 | 451 | 148 | BF468814 | BF468814 | UI-N-BH3- | |
| C 27 | 106.2 | 13.0 | 462 | 139 | BF755840 | BF755840 | 209890 | MA |
| C 28 | 105.4 | 12.9 | 507 | 116 | AW491608 | AW491608 | UI-N-BH3- | |
| C 29 | 105.2 | 12.8 | 537 | 168 | BF702273 | BF702273 | MI-P-A2-a | |
| C 30 | 103.6 | 12.6 | 537 | 168 | BF703127 | BF703127 | MI-P-A1-a | |
| C 31 | 103.4 | 12.6 | 532 | 168 | BF702078 | BF702078 | MI-P-A1-a | |
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| C 33 | 102.4 | 12.5 | 528 | 168 | BF712343 | BF712343 | MI-P-A3-a | |
| C 34 | 101.8 | 12.4 | 526 | 168 | BF702026 | BF702026 | MI-P-A1-a | |
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| C 36 | 100.8 | 12.3 | 534 | 168 | BF712419 | BF712419 | MI-P-A3-a | |
| C 37 | 100.2 | 12.2 | 537 | 168 | BF701994 | BF701994 | MI-P-A1-a | |
| 38 | 95.2 | 11.6 | 503 | 143 | BF074689 | BF074689 | 222166 | MA |
| C 39 | 93.2 | 11.4 | 530 | 168 | BF703911 | BF703911 | MI-P-A3-a | |
| C 40 | 91.6 | 11.2 | 433 | 161 | BE031109 | BE031109 | 129562 | MA |
| C 41 | 89 | 10.9 | 528 | 168 | BF712401 | BF712401 | MI-P-A3-a | |
| C 42 | 87.8 | 10.7 | 421 | 148 | BF442616 | BF442616 | 259514 | MA |
| 43 | 87.4 | 10.7 | 391 | 113 | AW313555 | AW313555 | 8811 | MARC |
| 44 | 85.2 | 10.4 | 378 | 113 | AW314907 | AW314907 | 11475 | MAR |
| C 45 | 84.2 | 10.3 | 526 | 168 | BF703280 | BF703280 | MI-P-A2-a | |

ALIGNMENTS

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| RESULT | 1 | |
| AC1308622 | 285 bp | mrna |
| LOCUS | | EST |
| DEFINITION | IpTR002 Channel catfish pituitary library Ictalurus punctatus cDNA clone IpTR002 5' similar to growth hormone, mRNA sequence. | |
| ACCESSION | AI308622 | |
| VERSION | AI308622.1 | GI:4003257 |
| KEYWORDS | EST. | |
| SOURCE | channel catfish. | |
| ORGANISM | Ictalurus punctatus | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus. | |
| AUTHORS | Liu,Z., Tan,G., Li,P. and Dunham,R. | |
| TITLE | Transcribed dnuceotide microsatellites and their associated genes from channel catfish, Ictalurus punctatus | |
| JOURNAL | Unpublished (1999) | |
| COMMENT | Other_ESTs: IpTR002u Contact: Liu, Z.J. Fish Molecular Genetics and Biotechnology Auburn University 203 Swingle Hall, Department of Fisheries, Auburn, AL 36849, USA Tel: 334 844 4054 Fax: 334 844 9208 Email: zliu@acesag.auburn.edu Seq primer: M13 reverse High quality sequence stop: 285. | |
| FEATURES | Location/Qualifiers | |
| source | 1..285 /organism="Ictalurus punctatus" /strain="Kansas" /db_xref="taxon:7998" /clone="IpTR002" /clone_lib="Channel catfish pituitary library" /sex="female" /tissue_type="pituitary" /dev_stage="adult" | |
| BASE COUNT | 64 a | 77 c 80 g 64 t |
| ORIGIN | | |

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| Query Match | 18.0%; | Score | 147.2; | DB | 18; | Length | 285; |
| Best Local Similarity | 80.1%; | Pred. | No. 3.7e-31; | | | | |
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| Db | 130 | GCCARAGATGGACCACTTTGAGAGAAGCTCTGTGTCCTGGAAGACGCAACAGCTGAGC | 189 |
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| Qy | 376 | AAAATCTTCCCCTGTGCTTTCTGCAATTCTGACTCATATTGAGCGGCCCTGCTGAAAAAGAT | 435 |
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| Qy | 436 | GAACACAGAGAGAGCTCTATGCTGAAGCTTCTTTCCG | 471 |
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| Db | 250 | GAGGCCAGAAAAGCTCTGTGCTGAAACTGCTGCAC | 285 |
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|-------------|---|
| RESULT | 2 |
| BE755837 | |
| LOCUS | BE755837 570 bp mRNA EST |
| DEFINITION | 209884 MARC 2BOV Bos taurus cDNA 5', mRNA sequence. |
| 15-SEP-2000 | |

RESULT 2

BE755837 570 bp mRNA EST 15-SEP-2000
 LOCUS 209884 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION
 ACCESSION BE755837
 VERSION BE755837.1 GI:10169901
 KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 570)
 Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
 Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
 ,W.W. and Keele,J.W.
 Design and use of four pooled tissue normalized cDNA libraries for
 EST discovery in cattle
 Unpublished (2000)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 1
 and -mismatch 12 options.

FEATURES

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/clone_lib="MARC-2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
119 a 180 c 158 g 113 t
BASE COUNT
ORIGIN

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| Query Match | 18.0% | Score 147.2; | DB 139; | Length 570; |
| Best Local Similarity | 55.7% | Pred. No. 4.6e-31; | | |
| Matches 303; | Conservative | 0; | Mismatches 238; | Indels 3; |
| | | | | Gaps 1; |

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QY 326 TTAAGCACTTTGAGACACCTCTGTTGCCCTGAGAACGACGACAGCTGAGTAAATCTTCC 385
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Db 150 AGTTGCTCTTCTGCTTCTGAAACATCCCGGCCCCACGGGCAAGAATGAGGCCAGC 209
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QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTTTTCACCTCATTTGAGTCTCTGGAGTTCC 505
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Db 210 AGAATCAGACTTGGAGCTGCTTCGCATCTCACTGCTCTCATCCAGTCTGCTGGCTGGGC 269
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QY 626 ATGTTCAACCAACATGATGATACAGACTCTCTTCCCGCTGCTTTTGAGGACTTCTACT 685
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Db 390 ATGGACCCCGGGCTGGGAGATCTCTCAAGCAGCTATGACAAATTTGACACAAACA 449
  || || || || || || || || || || || || || || || || || || || || ||
QY 686 TGACCATGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGCTGCTTCAAGAAGG 745
  || || || || || || || || || || || || || || || || || || || || ||
Db 450 TGGCGA---GTGACGACGCTGCTCAAGAACTACGGTCTGCTCTCTCTCCGGAAGG 506
  || || || || || || || || || || || || || || || || || || || || ||
QY 746 ACATGCAACAAGTCAGACCTACTTACGAGTTGAGGTTGCAAAATTCAGAGGATCCCTGGATTCCA 805
  || || || || || || || || || || || || || || || || || || || || ||
Db 507 ACCTGCTAAGACGAGAGCTACCTCGGGTCATGAAGTGGCGGCTTCGGGGAGGCCA 566
  || || || || || || || || || || || || || || || || || || || || ||
QY 806 ACTG 809
  || || || || || || || || || || || || || || || || || || || || ||
Db 567 GCTG 570
  || || || || || || || || || || || || || || || || || || || || ||

RESULT 3
AI308623/c
LOCUS
DEFINITION I308623u Channel catfish pituitary library Ictalurus punctatus cDNA
clone iptr002 3' similar to growth hormone, mRNA sequence.
ACCESSION
VERSION AI308623
KEYWORDS EST.
SOURCE channel catfish.
ORGANISM Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Siluriformes; Ictaluridae; Ictalurus.
REFERENCE
1 (bases 1 to 280)
Liu,Z., Tan G., Li,P. and Dunham,R.
Transcribed dinucleotide microsatellites and their associated genes
from channel catfish, Ictalurus punctatus
Unpublished (1999)
Other ESTs: Iptr002
Contact: Liu, Z.J.
Fish Molecular Genetics and Biotechnology
Auburn University
203 Swingle Hall, Department of Fisheries, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: M13 forward
High quality sequence stop: 280.
Location/Qualifiers
1. .280
/organism="Ictalurus punctatus"

QY 618 ATGCTCTGATGTTCAACCAACATGATGATTAACGACTCTTCCCGCTGCTTTTGAGGA 677
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Db 279 ATGCTGTGATGACAAACCGGCTGATGAGAACGACTCTCTAGCTCCGCTTTTCGAGGA 220
  || || || || || || || || || || || || || || || || || || || || ||
QY 678 CTTCTACTTGCACATGGGGAGAACACCTCAGAGAGAGCTTTCGCTGCTGCTGCTT 737
  || || || || || || || || || || || || || || || || || || || || ||
Db 219 TTTCTACCAAGCTTTCAGCGAGGAAACCTGAGGAAGAGCTTCGCTGCTGCTGCTT 160
  || || || || || || || || || || || || || || || || || || || || ||
QY 738 CAAGAGGACATGCACAAAGTCAGACCTACTTTCAGGGTTGCAAAATTCAGAGGATCCCT 797
  || || || || || || || || || || || || || || || || || || || || ||
Db 159 CAAGAGGACATGCACAAAGTCAGACCTACTTTCAGGGTTGCAAAATTCAGAGGATCCCT 100
  || || || || || || || || || || || || || || || || || || || || ||
QY 798 GGATTCCAACTGCACCTGTAG 819
  || || || || || || || || || || || || || || || || || || || || ||
Db 99 GGATTCCAACTGCACCTGTAG 78
  || || || || || || || || || || || || || || || || || || || || ||

RESULT 4
BE755987
LOCUS
DEFINITION 209988 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE755987
VERSION BE755987.1 GI:10169979
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoides;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 517)
Smith,T.P.B., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
EST Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemall.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 58 row: 0 column: 7
Seq primer: ATTTAGTGCACATATAG.
Location/Qualifiers
1. .517
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
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Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium.

BASE COUNT 110 a 165 c 137 g 105 t

Query Match 15.7%; Score 128.4; DB 139; Length 517;
Best Local Similarity 55.3%; Pred. No. 9.9e-26;
Matches 271; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

QY 266 GGCTCTTCAATATGACGATTCGTGTACACACCTGCACACCTGGCTGCAAAATGA 325
DB 30 GCCTGTTGCCAACGCTGTGCTCGGGCTCAGCACCTGCATCAGCTGGCTGCACACCT 89
QY 326 TTAAGCACTTTGAGGACACCTGTTGCCCTGAGGAACGACAGCTGAGTAATCTTCC 385
DB 90 TCAAGAGTTTGAGCGCACTACATCCCGGAGGACAGAGATACTCCATCCAGAACACCC 149
QY 386 CTCCTGCTTTCTGCAATTCGTACTACATTTGAGCGGCTGCTGAAAGATGAAACACAGA 445
DB 150 AGGTTGCCCTTCTGCTCTGAAACCATCCCGGCCCCACGGGCAAGATGAGGCCAGC 209
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTTTTACACCTCATTTGAGTCTCTGGAGTTCC 505
DB 210 AGAAATCAGACTTGGAGCTGCTTGCATCTCACTGCTCCTCATCCAGTCTGTGGCTTGGGC 269
QY 506 CAAGCCAGCTCCTGAGCGAACCGTCTCAACAGACCTGACCGTAGGAAACCCCAACAGC 565
DB 270 CCCTCAGTCTCCTGACGAGAGTCTTCAACACAGCTTGTGTGTCACCTCGGACCGTG 329
QY 566 TCACCTGAGAAGCTGGCGGACTTTGAAATGGGACATGATGCTGCTATCCAGGACATGCTCG 625
DB 330 TCTATGAGAGCTGAAGACCTTGGAGAGGACATCTGCGCCCTGATCGGGAGCTGGAAG 389
QY 626 ATGGTCAACCAACATGATGATTAACGACTCTCTTGCCTGCTGCTTTTGGAGCTTCTACT 685
DB 390 ATGGCACCCCGGGCTGGGACAGATCTTCAAGCAGACCTATGACAAATTTGACACAACA 449
QY 686 TGACCATGGGGAGAACACCTCAGAGAGCTTTCGTCTGCTGGCTGCTTCAAGAAGG 745
DB 450 TCGCGA---GTGACGACGGCTGCTCAAGAAGTACGCTGCTGCTCTCTGCTTCCGGAAG 506
QY 746 ACATGCACAA 755
DB 507 ACCTGCATAA 516

RESULT 5
LOCUS AW659506 547 bp mRNA EST 14-JUL-2000
DEFINITION 96738 MARC 1B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW659506
VERSION AW659506.1 GI:7425333
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 547)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov

Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCCGACGACGACG
Plate: 74 row: B column: 7
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source

1..547
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

BASE COUNT 101 a 183 c 149 g 114 t
ORIGIN

Query Match 15.1%; Score 124; DB 118; Length 547;
Best Local Similarity 58.8%; Pred. No. 1.8e-24;
Matches 214; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 266 GGCTCTTCAATATGACGATTCGTGTACACACCTGCACACCTGGCTGCAAAATGA 325
DB 147 GCCTGTTGCCAACGCTGTGCTCGGGCTCAGCACCTGCATCAGCTGGCTGCTGACACCT 206
QY 326 TTAACGACTTTGAGGACAGCTGTGCTGAGGAACGACAGACCTGAGTAAATCTTCC 385
DB 207 TCAAGAGTTTGAGCGCACCTATATCCGGAGGAGAGAGATATCTCATCCAGACACCC 266
QY 386 CTCCTGCTTTCTCAATTCGTACTACATTTGAGGCGCTGCTGGAAGATGAACACAGA 445
DB 267 AGGTGCTTCTGCTTCTCTGTAACCATCCCGGCCCGGCAAGATGAGGCCAGC 326
QY 446 AGAGCTCTATGATGAGCTTCTTCCGATCTCTTTACCTCATTTGAGTCTGGGAGTTCC 505
DB 327 AGAAATCAGACTTGGAGCTGCTTCCGATCTCACTGCTCTCATCCAGTCTGGCTTGGGC 386
QY 506 CAAGCCAGTCCCTGAGCGGAACCTCTCAACACCTGACCGTAGGAACCCCAACACAGC 565
DB 387 CCTGAGAGCTTCCAGCAGAGTCTTCAACACAGCTTGGTGTGGCACCTCGGACCTGTG 446
QY 566 TCACCTGAGAAGCTGGCGGACTTGAAATGGGCATCAGTGTGCTCATCCAGGACATGCTCG 625
DB 447 TCTATGAGAAGCTGAAGGACCTGGAGGAGGACATCTTGGCCCTGATCGGGAGCTGGAAG 506
QY 626 ATGG 629
DB 507 ATGG 510

RESULT 6
LOCUS BF077176 547 bp mRNA EST 18-OCT-2000
DEFINITION 226992 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF077176
VERSION BF077176.1 GI:10871006
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 547)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle

JOURNAL
COMMENT

Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGAGC
Plate: 89 row: J column: 7
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source

Location/Qualifiers
1. .547
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
101 a 183 c 149 g 114 t

Query Match 15.1%; Score 124; DB 143; Length 547;
Best Local Similarity 58.8%; Pred. No. 1.8e-24;
Matches 214; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 266 GGCTCTTCAATAATGACGATTCGTGTACAAACCTGCACACAGCTGGCTGCAAAAATGA 325

DB 146 GCCTGTTGCCAACGCTGTGCTCGGGCTCAGCACCTGCATGCTGCTGACACCT 205

QY 326 TTAACGACCTTCAGACAGCTGTTCCCTGAGGAAACGACAGCTGAGTAAATCTTCC 385

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QY 386 CTCTCTTCTGCAATTCGACTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 445

DB 266 AGTTGCTCTTCTGCTCTTCTGCTCTTCTGCTCTTCTGCTCTTCTGCTCTTCTGCT 325

QY 446 AGAGCTCTATGCTGAGCTTCTTTCGATCTCTTTCACCTCATTTGAGTCTCTGAGTCTCC 505

DB 326 AGAATCAGACTTGGAGCTGCTTCCGATCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 385

QY 506 CAAGCAGTCCCTGAGCGGAAACCGTCTCAACAGCCTGACCGTAGGAAACCCCAACG 565

DB 386 CCTGCTGCTCTGAGCGGAAACCGTCTCAACAGCCTGACCGTAGGAAACCCCAACG 445

QY 566 TCATGAGAGCTGCGGCGCTTCAAAATGGGATCAGTGTGCTCATCCAGGATGTCTCG 625

DB 446 TCTATGAGAGCTGAGGAGCTGGAGGAGGATCTCTGCGCCCTGATGCGGGAGCTGGA 505

QY 626 ATGG 629

DB 506 ATGG 509

RESULT 7

BE756195 BE756195 553 bp mRNA EST 15-SEP-2000
LOCUS 210269 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BE756195
ACCESSION BE756195
VERSION BE756195.1 GI:10170187
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

1 (bases 1 to 553)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,
W.W. and Keeler, J.W.

TITLE

Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle

JOURNAL

Unpublished (2000)

COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCACAGTCACGAGC

Plate: 60 row: M column: 12

Seq primer: ATTTAGGTGACACTATAG.

FEATURES

Location/Qualifiers
1. .553
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
105 a 184 c 150 g 114 t

Query Match 15.1%; Score 124; DB 139; Length 553;
Best Local Similarity 58.8%; Pred. No. 1.8e-24;
Matches 214; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 266 GGCTCTTCAATAATGACGATTCGTGTACAAACCTGCACACAGCTGGCTGCAAAAATGA 325

DB 146 GCCTGTTGCCAACGCTGTGCTCGGGCTCAGCACCTGCATGCTGCTGACACCT 205

QY 326 TTAACGACCTTGGAGGAGAGCTGTTCCCTGAGGAAACGACAGCTGAGTAAATCTTCC 385

DB 206 TCAAGAGTTTGAGCGCCTACATCCCGGGGAGAGAGATCTCCATCCAGAACCC 265

QY 386 CTCTGCTTCTGCAATTCGACTGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 445

DB 266 AGTTGCTCTTCTGCTCTTCTGCTCTTCTGCTCTTCTGCTCTTCTGCTCTTCTGCT 325

QY 446 AGAGCTCTATGCTGAGCTTCTTTCGATCTCTTTCACCTCATTTGAGTCTCTGAGTCTCC 505

DB 326 AGAATCAGACTTGGAGCTGCTTCCGATCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 385

QY 506 CAAGCAGTCCCTGAGCGGAAACCGTCTCAACAGCCTGACCGTAGGAAACCCCAACG 565

DB 386 CCTGCTGCTCTGAGCGGAAACCGTCTCAACAGCCTGACCGTAGGAAACCCCAACG 445

QY 566 TCATGAGAGCTGCGGCGCTTCAAAATGGGATCAGTGTGCTCATCCAGGATGTCTCG 625

DB 446 TCTATGAGAGCTGAGGAGCTGGAGGAGGATCTCTGCGCCCTGATGCGGGAGCTGGA 505

QY 626 ATGG 629

DB 506 ATGG 509

RESULT 8

AW631765

LOCUS AW631765 576 bp mRNA EST 14-JUL-2000
DEFINITION 91039 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW631765
VERSION AW631765.1 GI:7388845
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 576)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGCG
Plate: 76 row: L column: 20
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..576
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
BASE COUNT 113 a 189 c 155 g 119 t
ORIGIN
Query Match 15.1%; Score 124; DB 118; Length 576;
Best Local Similarity 58.8%; Pred. NO. 1.8e-24;
Matches 214; Conservative 0; Mismatches 150; Indels 0; Gaps 0;
QY 266 GGCTCTTCAATAATCAGTCATTGCTGTACACACCTGCACACGCTGGCTGCAAAATGA 325
DB 147 GCCTGTTGGCCAACTGTGCTCGGGGCTCAGCACCTGCATCGCTGCTGACACCT 206
QY 326 TTAAGGACTTTGAGGACGCTGTTGCCCTGAGGACGACGACGCTGAGTAAATCTTCC 385
DB 207 TCAAGAGTTTGAGCGACCTACATCCCGGAGGACAGAGATACTCCATCCAGAACACCC 266
QY 386 CTCTGCTTTCTGCAATTTCTGACTACTTGGAGCGCTGCTGGAAGAAGTAAACACAGA 445
DB 267 AGGTTGCCCTTCTGCTTCTGTAACCATCCCGCCCCCAGGCAAGATAGGCCACCG 326
QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTTTTTCACCTCAATGAGTCTCTGGAGTTCC 505
DB 327 AGAATCAGACTTGAGGCTGCTTCGATCTCTCACTGCTCCTCATCCAGTCTGCTGGGCT 386
QY 506 CAAGCCAGTCTGAGCGGAACCGCTCAACACAGCTGACCTAGGACCCCAACCCAGC 565
DB 387 CCTGCACTTCTCAGCAGAGTCTTACCAACAGAGCTTGCTGTTGGACCTCGGACCGTG 446
QY 566 TCACTGAGAAGCTGCCGCACTTGAATAGGGCATCAGTGTGCTCATCCAGGCACTGCTCG 625
DB 447 TCTATGAGAAGCTGAAGACCTGGAGGAGGATCCTGGCCCTGATGGGAGCTGGAG 506

QY 626 ATGG 629
DB 507 ATGG 510
RESULT 9
BF605397 497 bp mRNA EST 13-DEC-2000
LOCUS 271754 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION BF605397
ACCESSION BF605397
VERSION BF605397.1 GI:11704971
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 497)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGCG
Plate: 55 row: E column: 9
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..497
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 90 a 167 c 134 g 106 t
ORIGIN
Query Match 15.1%; Score 123.8; DB 150; Length 497;
Best Local Similarity 59.5%; Pred. NO. 2e-24;
Matches 209; Conservative 0; Mismatches 142; Indels 0; Gaps 0;
QY 266 GGCTCTTCAATAATCAGTCATTGCTGTACACACCTGCACACGCTGGCTGCAAAATGA 325
DB 142 GCCTGTTGGCCAACTGTGCTCGGGCTCAGCACCTGCATCGCTGCTGACACCT 201
QY 326 TTAACGACTTTGAGGACGCTGTTGCCCTGAGGACGACGACGCTGAGTAAATCTTCC 385
DB 202 TCAACAGTTTGAGCGCACCTACATCCCGGAGGACAGAGATACTCCATCCAGAACACCC 261
QY 386 CTCTGCTTTCTGCAATTTCTGACTACTTGAAGCGCTGCTGGAAGAAGTAAACACAGA 445
DB 262 AGGTTGCCCTTCTGCTTCTGTAACCATCCCGCCCCCAGGCAAGATAGGCCACCG 321
QY 446 AGAGCTCTATGCTGAAGCTTCTTTCGATCTTTTTCACCTCATTTGAGTCTCTGGAGTTCC 505
DB 322 AGAATCAGACTTGAGGCTGCTTCCGATCTCACTGCTCTCCATCCAGCTGCTGGGCT 381

```

QY 506 CAAGCAGTCCCTGAGCGGACCGTCTCAACAGAGCTGACGCTAGGGAAACCCCAACAGC 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 CCCTGAGTTCCTCAGCAGAGTCTTCCACACAGCTGGTGTGGGACCTCGGACCGTG 441

QY 566 TCACTGAGAAGCTGGCGGACGCTGAAAATAGGCGATGCTGCTCATCCAGG 616
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Db 442 TCTATGAGAAGCTGAAGAGCCTGAGGAAAGGCATCCTCGGCCCTGATGGGG 492

RESULT 10
LOCUS BF655271 477 bp mRNA EST 20-DEC-2000
DEFINITION 279722 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF655271
VERSION BF655271.1 GI:11920403
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 477)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrnerkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid
, W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGACGACGAGC
Plate: 75 row: H column: 11
Seq primer: ATTAGCTGACACTATAG.
Location/Qualifiers
1..477
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
87 a 160 c 127 g 103 t

BASE COUNT
ORIGIN

Query Match 14.7%; Score 120.6; DB 151; Length 477;
Best Local Similarity 60.0%; Pred. No. 1.6e-23;
Matches 201; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 266 GCCTCTTCAATATGAGTCTATTCGTGTACACACCTGCACAGCTGCTGCAAAAATGA 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 138 GCCTGTTCACCAAGCTGTGCTCGGGCTCAGCACCTGCATCAGCTGGCTGTGACACCT 197

QY 326 TTACGACTTTGAGACAGCTGTGCTGTAGGACGCGACAGCTGAGTAAATCTTCC 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 198 TCAAGAGTTTTSAGCGGACCTTACATCCCGGAGGACAGAGATACCTCCACAGAACCCC 257

QY 386 CTCGTCTTCTTCAATCTCAGTACATTTAGGCGCTGTGGAAAGATGAACACACAGA 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 258 AGGTGGCTTCTCTCTCTGAACCACTCCCGGGCCCCCAGGCAAGTAGGAGCCACG 317

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QY 446 AGAGCTCTATGCTGAAGCTTCTTCGCATCTCTTTTACCTCATGCTGAGTCTGGAGTTCC 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 318 AGAANTCAGACTTGGAGCTGCTTCGCATCTCACTGCTCTCATCCAGTCTGCTTGGGC 377

QY 506 CAAGCAGTCCCTGAGCGGAAACCGTCTCAACAGAGCTGACCGTAGGAAACCCCAACAGC 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 378 CCCTCAGTTCCTCAGCAGAGTCTTCCACACAGCTGTGGTGTGGCAGCTGGACCGTG 437

QY 566 TCACTGAGAAGCTGGCGGACGCTGAAAATGGGCATC 600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 438 TCTATGAGAAGCTGAAGGACCTGGAGGAGGCATC 472

RESULT 11
LOCUS BE861283 476 bp mRNA EST 29-SEP-2000
DEFINITION UI-M-AJ1-ahh-h-03-0-UI.r1 NIH_BMAP_MOB_N Mus musculus cDNA clone
UI-M-AJ1-ahh-h-03-0-UI 5', mRNA sequence.
ACCESSION BE861283
VERSION BE861283.1 GI:10379077
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 476)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
collaborative arrangements
Seq primer: M13 Reverse.
Location/Qualifiers
1..476
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="NIH_BMAP_MOB_N"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_MOB_N library is a normalized library constructed
from mouse olfactory bulbs. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories."
99 a 148 c 125 g 104 t

BASE COUNT
ORIGIN

Query Match 14.4%; Score 117.6; DB 140; Length 476;
Best Local Similarity 57.7%; Pred. No. 1.1e-22;
Matches 210; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 266 GCCTCTTCAATATGAGTCTATTCGTGTACACACCTGCACAGCTGCTGCAAAAATGA 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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| | | | |
|----|-----|--|-----|
| QY | 550 | GGAAACCCCAACAGCTCACTAGAGAGCTGGCCGACTTGAAATGGGCATCAGTGTGCTC | 609 |
| Db | 2 | GGCACTTAAACATATCGCAGAGAGCTGGTGACTCGT- AAATGGGCATCGCGCTACTT | 60 |
| QY | 610 | ATCAGGCGATGTCCTCATGGTCAACCAACATGGATGAATACGACTCCTTGGCGCTGCCT | 669 |
| Db | 61 | ATCGAGGAGTGTGTAGCAAAACCGCGCTGGTAGAACAGCTCTCTGGCTCGCC- | 119 |
| QY | 670 | TTTGAGGACTTCTACTTGACCATGGGGGAGAACAACTCAGAGAGAGCTTTCGTCT- GCT | 728 |
| Db | 120 | TTTCAGGAGATTCTTACCAGAGACCTTGACGAGAGGAAACCTCAGGAAGAGCTTCGCTCTGGCT | 179 |
| QY | 729 | GGCTGCTCTCAGAAGGACATGCACAAAGTCGAGAGCTACTCTGAGGGTTGCAAAATTCAG | 788 |
| Db | 180 | GTCTGCTTCAAGAGGACATGCACAAAGGTGAGAGCTTCTGAGGCGTGGCCAAAGTGCAG | 239 |
| QY | 789 | GAGATCCCTGGATTCCAATGC | 810 |
| Db | 240 | GAGTACTCGGTTACCAACCTGC | 261 |

| | |
|------------|--|
| RESULT | 13 |
| AUI70721/c | |
| LOCUS | AUI70721 697 bp mRNA |
| DEFINITION | AUI70721 Ol-br-ad cDNA Oryzias latipes EST clone br6804, mRNA sequence. |
| | 29-JAN-2001 |

| FEATURES | source | BASE COUNT | ORIGIN |
|-------------|-----------------------------|------------|----------|
| (3' -> 3'). | Location/Qualifiers | 173 a | 1 others |
| 1. .697 | /organism="Oryzias latipes" | 149 c | 204 t |
| | /strain="HNI" | | |
| | /db_xref="taxon:8090" | | |
| | /clone="br5604" | | |
| | /clone_lib="Ol-br-ad CDNA" | | |
| | /sex="female/male mixed" | | |
| | /tissue_type="brain" | | |
| | /dev_stage="adult" | | |

[illegible]

Search completed: May 16, 2001, 09:43:34
Job time: 4322 sec